

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 2, 2001, 10:35:51 ; Search time 62.83 Seconds
(without alignments)
27.982 Million cell updates/sec

Title: US-09-273-217-1

Perfect score: 78
Sequence: 1 FAFADERDSQFPSP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.15:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.protist:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	141	6	009074 sus scrofa
2	78	100.0	476	6	008635 bos taurus
3	78	100.0	499	6	09MX3 oryctolagus
4	74	94.9	123	6	09N0E4 sus scrofa
5	74	94.9	141	6	009075 sus scrofa
6	74	94.9	499	6	028293 canis fam1
7	67	85.9	277	6	009076 oryctolagus
8	67	85.9	277	6	09TUK6 oryctolagus
9	67	85.9	279	6	009080 oryctolagus
10	67	85.9	279	6	09TUK7 oryctolagus
11	67	85.9	286	6	002911 oryctolagus
12	60	76.9	529	11	061923 mus musculu
13	59	75.6	494	13	091830 oncorhynch
14	57	73.1	260	6	009079 oryctolagus
15	54	69.2	955	5	076805 drosophila
16	51	65.4	575	11	09Q0U4 Q9qu4 rattus sp.
17	51	65.4	857	11	003717 mus musculu
18	51	65.4	858	4	014193 homo sapien
19	51	65.4	858	6	018868 sus scrofa

20	51	65.4	858	6	09M219 oryctolagus
21	51	65.4	876	13	091593 xenopus lae
22	50	64.1	489	13	091781 xenopus lae
23	51	64.1	511	4	016322 homo sapien
24	50	64.1	725	6	028649 oryctolagus
25	49	62.8	482	5	009937 caenorhabdi
26	49	62.8	483	13	091829 oncorhynch
27	49	62.8	593	6	028248 canis fam1
28	49	62.8	602	11	0921R6 mus musculu
29	48	61.5	27	13	073608 gallus gall
30	47	60.3	27	13	073609 gallus gall
31	47	60.3	662	13	09YX8 gallus gall
32	46	59.0	516	6	028656 oryctolagus
33	45	57.7	532	11	070259 mus musculu
34	45	57.7	597	6	09T507 bos taurus
35	44	56.4	488	5	025376 sus scrofa
36	44	56.4	905	5	026344 aplysia sp.
37	43	55.1	515	5	016968 aplysia cal
38	43	55.1	898	13	091592 xenopus lae
39	42	53.8	460	5	009658 caenorhabdi
40	42	53.8	512	5	026597 schistosoma
41	41	52.6	136	6	009077 sus scrofa
42	41	52.6	374	2	09S3X6 streptomyce
43	41	52.6	478	5	091784 polychaen
44	40	51.3	41	4	09UD44 homo sapien
45	40	51.3	260	6	09XSQ0 oryctolagus

ALIGNMENTS

RESULT 1
ID 009074 PRELIMINARY: PRT: 141 AA.
AC 009074:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE POTASSIUM CHANNEL PROTEIN (CLONE LLC2) (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92125505; PubMed=1733291;
RA Desir G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,
RA Igarashi P.;
RT *Isolation of putative voltage-gated epithelial K-channel isoforms
from rat kidney and LLC-PK1 cells.";
RL Am J Physiol. 262:151-157(1992).
RT
CC -I- FUNCTION: THIS PROTEIN IS INVOLVED IN RENAL EPITHELIAL TRANSPORT
AND MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF
MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO
THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A
POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN
ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
EVERY THIRD POSITION.
CC -I- SIMILARITY: BELONGS TO THE SHAKER-RELATED POTASSIUM CHANNEL
SUBFAMILY 1.
CC INTERPRO: IPR000636; -
DR INTERPRO: IPR001622; -
DR INTERPRO: IPR003091; -
DR PFAM: PF00520; ion.trans. 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family.
FT NON_TER 1 6 SEGMENT S3.
FT TRANSMEM <1 41 SEGMENT S4.
FT TRANSMEM 23 41

FT TRANSMEM 58 77 SEGMENT S5.
 FT TRANSMEM 119 141 SEGMENT S6.
 FT NON_TER 141 141
 SO SEQUENCE 141 AA; 15342 MW; C20E9B3BB1412340 CRC64;

Query Match 100.0%; Score 78; DB 6; Length 141;
 Best Local Similarity 100.0%; Pred. No. 6; 2e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEDERDSOPSP 15
 Db 78 FAEDERDSOPSP 92

RESULT 2

008635 PRELIMINARY; PRT: 476 AA.

AC 008635; 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE POTASSIUM CHANNEL PROTEIN KVL.2 (BGR5) (FRAGMENT).

OS Bos taurus (Bovine); Chordata; Vertebrata; Euteleostomi;

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RP SEQUENCE FROM N.A.

RX MEDLINE=92267180; PubMed=1587348;

RA Reid P.F., Pongs O., Dolly J.O.;

RT "Cloning of a bovine voltage-gated K⁺ channel gene utilizing partial amino acid sequence of a dendrotoxin-binding protein from brain cortex."

RL FEBS Lett. 302:31-34(1992).

CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

CC -1- MISCELLANEOUS: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.

CC -1- SIMILARITY: BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.

DR EMBL; X66185; CAA46953.1; -

DR INTERPRO: IPR000636; -

DR INTERPRO: IPR001622; -

DR INTERPRO: IPR003091; -

DR INTERPRO: IPR003131; -

DR PIRAM: PF00520; Ion_trans; 1.

DR PIRAM: PF02214; K_tetra; 1.

DR PRINTS: PR00169; KCHANNEL.

KM Glycoprotein; Multigene family; Ion transport; Voltage-gated channel;

FT TRANSMEM 164 182 SEGMENT S1 (BY SIMILARITY).

FT TRANSMEM 222 243 SEGMENT S2 (BY SIMILARITY).

FT TRANSMEM 255 275 SEGMENT S3 (BY SIMILARITY).

FT TRANSMEM 293 311 SEGMENT S4 (BY SIMILARITY).

FT TRANSMEM 328 347 SEGMENT S5 (BY SIMILARITY).

FT TRANSMEM 389 411 SEGMENT S6 (BY SIMILARITY).

FT MOD_RES 449 449 PHOSPHORYLATION (BY CAPK) (BY SIMILARITY).

FT CARBOHYD 38 38 POTENTIAL.

FT CARBOHYD 207 207 POTENTIAL.

FT NON_TER 476 476

SO SEQUENCE 476 AA; 54152 MW; D350456A611C057D CRC64;

Query Match 100.0%; Score 78; DB 6; Length 476;
 Best Local Similarity 100.0%; Pred. No. 2; 3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEDERDSOPSP 15
 Db 348 FAEDERDSOPSP 362

RESULT 3

09MYX3 PRELIMINARY; PRT: 499 AA.

AC 09MYX3; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE POTASSIUM CHANNEL SUBUNIT KV 1.2.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RP SEQUENCE FROM N.A.

RA Thorndike K.S., Walsh M.P., Cole W.C.;

RT "Rabbit portal vein kv 1.2."

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF284420; AAF91476.1; -

SO SEQUENCE 499 AA; 56692 MW; 7A4BF468FB36308 CRC64;

OY 1 FAEDERDSOPSP 15
 Db 348 FAEDERDSOPSP 362

RESULT 4

09NOE4 PRELIMINARY; PRT: 123 AA.

AC 09NOE4; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE VOLTAGE-DEPENDENT K CHANNEL (FRAGMENT).

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RP SEQUENCE FROM N.A.

RA Onya S., Imazumi Y.;

RT "porcine voltage-dependent K channel (Kv1.2)."

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB043552; BAB07847.1; -

FT NON_TER 123 123

SO SEQUENCE 123 AA; 13532 MW; 232096561F6D3461 CRC64;

Query Match 94.9%; Score 74; DB 6; Length 123;
 Best Local Similarity 93.3%; Pred. No. 3e-06;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEDERDSOPSP 15
 Db 25 FAEDERDSOPSP 39

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RESULT 5
ID 009075 PRELIMINARY: PRT: 141 AA.
AC 009075:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE POTASSIUM CHANNEL PROTEIN (CLONE LLC1) (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92125505; PubMed=1733291;
RA Desir G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,
RA Igarashi P.;
RT "Isolation of putative voltage-gated epithelial K-channel isoforms
RT from rabbit kidney and LLC-PK1 cells.";
RL Am. J. Physiol. 262:151-157(1992)
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN RENAL EPITHELIAL TRANSPORT
CC AND MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF
CC MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO
CC THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A
CC POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN
CC ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: BELONGS TO THE SHAKER-RELATED POTASSIUM CHANNEL
CC SUBFAMILY 1.
CC INTERPRO: IPR000636; -
CC DR INTERPRO: IPR001622; -
CC DR INTERPRO: IPR003091; -
CC PFAM: PF00520; Ion_trans. 1.
CC PRINTS: PR00169; KCHANNEL.
CC DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family.
FT NON_TER 1
FT TRANSMEM <1 6 SEGMENT S3.
FT TRANSMEM 23 41 SEGMENT S4.
FT TRANSMEM 58 77 SEGMENT S5.
FT TRANSMEM 119 141 SEGMENT S6.
FT NON_TER 141
SQ SEQUENCE 141 AA; 15340 MW; 771ADPCGAB5255A CRC64;

Query Match 94.9%; Score 74; DB 6; Length 141;
Best Local Similarity 93.3%; Pred. No. 3.4e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEDERDSQPSIP 15
DB 78 FAEDERDSQPSIP 92
|||||:|||||
1 FAEDERDSQPSIP 15
|||||:|||||
78 FAEDERDSQPSIP 92

RESULT 6
ID 028293 PRELIMINARY: PRT: 499 AA.
AC 028293:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE DELAYED RECTIFIER K+ CHANNEL.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94022435; PubMed=8415758;
RA Hart P.J., Overturf K.E., Russell S.N., Carl A., Hume J.R.,

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RA Sanders K.M., Horowitz B.;
RT "Cloning and expression of a Kv1.2 class delayed rectifier K+ channel
RT from canine colonic smooth muscle.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:9659-9663(1993).
DR EMBL: L19740; AAA03607.1; -
DR INTERPRO: IPR000636; -
DR INTERPRO: IPR001622; -
DR INTERPRO: IPR003091; -
DR INTERPRO: IPR003131; -
DR PFAM: PF00520; Ion_trans. 1.
DR PFAM: PF02214; K_tetra. 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel.
SQ SEQUENCE 499 AA; 56606 MW; 394FDA7D04CABEC8 CRC64;

Query Match 94.9%; Score 74; DB 6; Length 499;
Best Local Similarity 93.3%; Pred. No. 1.3e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEDERDSQPSIP 15
DB 348 FAEDERDSQPSIP 362
|||||:|||||
1 FAEDERDSQPSIP 15
|||||:|||||
348 FAEDERDSQPSIP 362

RESULT 7
ID 009076 PRELIMINARY: PRT: 277 AA.
AC 009076:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE POTASSIUM CHANNEL PROTEIN (CLONE KC2) (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=KIDNEY;
RX MEDLINE=92125505; PubMed=1733291;
RA Desir G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,
RA Igarashi P.;
RT "Isolation of putative voltage-gated epithelial K-channel isoforms
RT from rabbit kidney and LLC-PK1 cells.";
RL Am. J. Physiol. 262:151-157(1992).
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN RENAL EPITHELIAL TRANSPORT
CC AND MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF
CC MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO
CC THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A
CC POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN
CC ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN, LIVER, KIDNEY.
CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
CC IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: BELONGS TO THE SHAKER-RELATED POTASSIUM CHANNEL
CC SUBFAMILY 1.
CC INTERPRO: IPR000636; -
CC DR INTERPRO: IPR003091; -
CC DR INTERPRO: IPR003131; -
CC PFAM: PF00520; Ion_trans. 1.
CC PFAM: PF02214; K_tetra. 1.
CC PRINTS: PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family.
FT NON_TER 1
FT TRANSMEM 83 101 SEGMENT S1.
FT TRANSMEM 141 162 SEGMENT S2.
FT TRANSMEM 174 193 SEGMENT S3.
FT TRANSMEM 206 224 SEGMENT S4.
FT TRANSMEM 241 260 SEGMENT S5.

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FT NON_TER 277 277
 SQ SEQUENCE 277 AA; 31819 MW; A991F1BF6A72C649 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 67; DB 6; Length 277;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAADERDSQFPS 13
 |||||||||||
 Db 265 FAADERDSQFPS 277

RESULT 8
 Q9TUK6 PRELIMINARY; PRT; 277 AA.

ID Q9TUK6
 AC Q9TUK6
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL ISOFORM 3 (FRAGMENT).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BREED NEW ZEALAND WHITE; TISSUE=KIDNEY;
 RX MEDLINE=92125505; PubMed=1733291;
 RA Desir G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,
 RA Igarashi P.,
 RT "Isolation of putative voltage-gated epithelial K-channel isoforms
 from rabbit kidney and LLC-PK1 cells.";
 RL Am. J. Physiol. 262:0-0(1992).
 DR EMBL: M81352; AAD43821.1; -
 DR INTERPRO: IPR000636; -
 DR INTERPRO: IPR003091; -
 DR PFM: PF00520; Ion_trans; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel.
 FT NON_TER 1 1
 FT SEQUENCE 277 AA; 31825 MW; 15FA32496FD8384 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 67; DB 6; Length 277;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAADERDSQFPS 13
 |||||||||||
 Db 265 FAADERDSQFPS 277

RESULT 9
 Q09080 PRELIMINARY; PRT; 279 AA.

ID Q09080
 AC Q09080
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE POTASSIUM CHANNEL PROTEIN (CLONE KC19) (FRAGMENT).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE=92125505; PubMed=1733291;
 RA Desir G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,
 RA Igarashi P.,
 RT "Isolation of putative voltage-gated epithelial K-channel isoforms
 from rabbit kidney and LLC-PK1 cells.";
 RL Am. J. Physiol. 262:0-0(1992).
 DR EMBL: M81351; AAD43820.1; -
 DR INTERPRO: IPR000636; -
 DR INTERPRO: IPR003091; -
 DR PFM: PF00520; Ion_trans; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel.
 FT NON_TER 1 1
 FT SEQUENCE 279 AA; 32022 MW; E942DCB864906982 CRC64;

RT from rabbit kidney and LLC-PK1 cells.";
 RL Am. J. Physiol. 262:151-157(1992).
 CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN RENAL EPITHELIAL TRANSPORT
 AND MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF
 MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO
 THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A
 POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN
 ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: BRAIN, LIVER, KIDNEY.
 CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
 IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 EVERY THIRD POSITION.
 CC -1- SIMILARITY: BELONGS TO THE SHAKER-RELATED POTASSIUM CHANNEL
 SUBFAMILY 1.
 DR INTERPRO: IPR000636; -
 DR INTERPRO: IPR003091; -
 DR INTERPRO: IPR003131; -
 DR PFM: PF00520; Ion_trans; 1.
 DR PFM: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family.
 FT NON_TER 1 1
 FT TRANSMEM 83 101 SEGMENT S1.
 FT TRANSMEM 141 162 SEGMENT S2.
 FT TRANSMEM 174 194 SEGMENT S3.
 FT TRANSMEM 211 229 SEGMENT S4.
 FT TRANSMEM 247 266 SEGMENT S5.
 FT CARBOHYD 126 126 POTENTIAL.
 FT NON_TER 279 279
 SQ SEQUENCE 279 AA; 32034 MW; E1E04D01746E896C CRC64;

Query Match
 Best Local Similarity 100.0%; Score 67; DB 6; Length 279;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAADERDSQFPS 13
 |||||||||||
 Db 267 FAADERDSQFPS 279

RESULT 10
 Q9TUK7 PRELIMINARY; PRT; 279 AA.

ID Q9TUK7
 AC Q9TUK7
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL ISOFORM 2 (FRAGMENT).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BREED NEW ZEALAND WHITE; TISSUE=KIDNEY;
 RX MEDLINE=92125505; PubMed=1733291;
 RA Desir G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,
 RA Igarashi P.,
 RT "Isolation of putative voltage-gated epithelial K-channel isoforms
 from rabbit kidney and LLC-PK1 cells.";
 RL Am. J. Physiol. 262:0-0(1992).
 DR EMBL: M81351; AAD43820.1; -
 DR INTERPRO: IPR000636; -
 DR INTERPRO: IPR003091; -
 DR PFM: PF00520; Ion_trans; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel.
 FT NON_TER 1 1
 FT SEQUENCE 279 AA; 32022 MW; E942DCB864906982 CRC64;

Query Match 85.9%; Score 67; DB 6; Length 279;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAERDERDSQFPS 13
 |||||||
 DB 267 FAERDERDSQFPS 279

RESULT 11
 ID 002911 PRELIMINARY; PRT: 286 AA.
 AC 002911;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE POTASSIUM CHANNEL PROTEIN (CLONE KC6) (FRAGMENT).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEW ZEALAND WHITE; TISSUE=KIDNEY;
 RX MEDLINE=93158774; PubMed=7679255;
 RA Desir G.V., Velazquez H.;
 RT "Identification of a novel K-channel gene (KC22) that is highly
 expressed in distal tubule of rabbit kidney.";
 RL Am. J. Physiol. 264:128-133(1993).
 CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN RENAL EPITHELIAL TRANSPORT
 MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF
 MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO
 THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A
 POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN
 ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: BRAIN AND TO A MUCH LESSER EXTENT, STOMACH,
 SPLEEN, KIDNEY, AND HEART.
 CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
 IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 EVERY THIRD POSITION.
 CC -1- SIMILARITY: BELONGS TO THE SHAKER-RELATED POTASSIUM CHANNEL
 SUBFAMILY 1.
 CC EMBL: L01789; AAA31380.1; -;
 DR INTERPRO: IPR000636; -;
 DR INTERPRO: IPR003091; -;
 DR INTERPRO: IPR003131; -;
 DR PIRAM: PF00520; Ion_trans; 1.
 DR PIRAM: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KM Glycoprotein; Multigene family.
 FT NON_TER 1
 FT TRANSMEM 86 106 SEGMENT S1.
 FT TRANSMEM 148 168 SEGMENT S2.
 FT TRANSMEM 180 203 SEGMENT S3.
 FT TRANSMEM 215 239 SEGMENT S4.
 FT TRANSMEM 252 275 SEGMENT S5.
 FT CARBOHYD 129 129 POTENTIAL.
 FT NON_TER 286
 SQ SEQUENCE 286 AA; 32446 MW; BED94DAD21E12A07 CRC64;

Query Match 85.9%; Score 67; DB 6; Length 286;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAERDERDSQFPS 13
 |||||||
 DB 274 FAERDERDSQFPS 286

RESULT 12
 ID 061923 PRELIMINARY; PRT: 529 AA.
 AC 061923;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE MORINE POTASSIUM CHANNEL PROTEIN.
 GN MK1.6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Migeon M.B., Street V.A., Demas V.P., Tempel B.L.;
 RL Epilepsy Res. 0:0-0(0).
 DR EMBL: M6688; AAA39772.1; -;
 DR INTERPRO: IPR000636; -;
 DR INTERPRO: IPR001622; -;
 DR INTERPRO: IPR003091; -;
 DR INTERPRO: IPR003131; -;
 DR PIRAM: PF00520; Ion_trans; 1.
 DR PIRAM: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel.
 SQ SEQUENCE 529 AA; 58673 MW; 336D78C069ABEADD CRC64;

Query Match 76.9%; Score 60; DB 11; Length 529;
 Best Local Similarity 80.0%; Pred. No. 0.0057;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAERDERDSQFPS 15
 |||||: |||||
 DB 396 FAERDDVSLFPSIP 410

RESULT 13
 ID 091830 PRELIMINARY; PRT: 494 AA.
 AC 091830;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE SHAKER-RELATED POTASSIUM CHANNEL TSHAL.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RX MEDLINE=98146169; PubMed=9486764;
 RA Nguyen T.D., Jeserich G.;
 RT "Molecular structure and expression of shaker type potassium channels
 in gill cells of trout CNS.";
 RL J. Neurosci. Res. 51:284-292(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RA Nguyen T.D., Jeserich G.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF252301; AAF70087.1; -;
 KW Ionic channel.
 SQ SEQUENCE 494 AA; 55899 MW; AF66998F97F22CD4 CRC64;

Query Match 75.6%; Score 59; DB 13; Length 494;
 Best Local Similarity 80.0%; Pred. No. 0.0082;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FAADERDSQFSP 15
 DB 343 FAADERDSQFSP 357

RESULT 14
 ID 009079 PRELIMINARY; PRT: 260 AA.

AC 009079: 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE POTASSIUM CHANNEL PROTEIN (CLONE KC10) (FRAGMENT).
 OS ORCTOLAGUS CULICULUS (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE=92125505; PubMed=1733291;
 RA Desir G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,
 RA Tigarshi P.;
 RT "Isolation of putative voltage-gated epithelial K-channel isoforms
 from rabbit kidney and LLC-PK1 cells.";
 RL Am. J. Physiol. 262:151-157(1992).
 CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN RENAL EPITHELIAL TRANSPORT
 AND MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF
 MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO
 THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A
 POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN
 ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
 IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 EVERY THIRD POSITION.
 CC -1- SIMILARITY: BELONGS TO THE SHAKER-RELATED POTASSIUM CHANNEL
 SUBFAMILY 1.
 CC INTERPRO: IPR000636; -;
 DR INTERPRO: IPR003091; -;
 DR INTERPRO: IPR003131; -;
 DR PFAM: PF00520; Ion_trans; 1.
 DR PFAM: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family.
 FT NON_TER 1 1
 FT TRANSMEM 85 103 SEGMENT S1.
 FT TRANSMEM 123 145 SEGMENT S2.
 FT TRANSMEM 156 176 SEGMENT S3.
 FT TRANSMEM 193 211 SEGMENT S4.
 FT TRANSMEM 228 247 SEGMENT S5.
 FT CARBOHYD 109 109 POTENTIAL.
 FT CARBOHYD 157 157 POTENTIAL.
 FT NON_TER 260 260
 SQ SEQUENCE 260 AA; 29833 MW; 829929930A9B7BFF CRC64;

Query Match 73.1%; Score 57; DB 6; Length 260;
 Best Local Similarity 84.6%; Pred. NO. 0.0097;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 FAADERDSQFSP 13
 DB 248 FAADERDSQFSP 260

RESULT 15
 ID 076805 PRELIMINARY; PRT: 955 AA.
 AC 076805:
 DT 01-NOV-1998 (Tremblrel. 08, Created)

DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE DELAYED RECTIFIER POTASSIUM CHANNEL.
 GN SHAB.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CANTON S;
 RA Hegde P., Gu G.G., Chen D., Free S.J., Singh S.;
 RT "Mutational analysis of the Shab gene in Drosophila.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF084525; AAC33365.1; -;
 DR INTERPRO: IPR000636; -;
 DR INTERPRO: IPR001622; -;
 DR INTERPRO: IPR003091; -;
 DR INTERPRO: IPR003131; -;
 DR PFAM: PF00520; Ion_trans; 1.
 DR PFAM: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel.
 SQ SEQUENCE 955 AA; 103132 MW; B245150FC90400CF CRC64;

Query Match 69.2%; Score 54; DB 5; Length 955;
 Best Local Similarity 66.7%; Pred. NO. 0.14;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FAADERDSQFSP 15
 DB 597 FAEKEDKTKFSP 611

Search completed: February 2, 2001, 10:39:07
 Job time: 196 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 2, 2001, 10:36:36 ; Search time 20.39 Seconds
(without alignments)
23.757 Million cell updates/sec

Title: US-09-273-217-1
Perfect score: 78
Sequence: 1 FAEADERDSQFPSP15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues
Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	499	1	CIR2_MOUSE
2	78	100.0	499	1	CIR2_XENLA
3	74	94.9	499	1	CIR2_HUMAN
4	61	78.2	529	1	CIR6_HUMAN
5	60	76.9	530	1	CIR6_RAT
6	56	71.8	273	1	CIR2_RABYT
7	54	69.2	924	1	CIRB_DROME
8	51	65.4	495	1	CIR1_HUMAN
9	51	65.4	495	1	CIR1_MOUSE
10	51	65.4	495	1	CIR1_RAT
11	51	65.4	853	1	CIR1_RAT
12	51	65.4	854	1	CIR1_HUMAN
13	49	62.8	601	1	CIR5_MOUSE
14	48	61.5	602	1	CIR5_MOUSE
15	48	61.5	602	1	CIR5_RAT
16	48	61.5	653	1	CIR4_HUMAN
17	48	61.5	654	1	CIR4_MOUSE
18	48	61.5	654	1	CIR4_MOUSE
19	48	61.5	655	1	CIR4_RAT
20	48	61.5	660	1	CIR4_BOVIN
21	46	59.0	523	1	CIR3_HUMAN
22	46	59.0	525	1	CIR3_RAT
23	46	59.0	528	1	CIR3_MOUSE
24	46	59.0	598	1	CIR5_RABIT
25	46	59.0	613	1	CIR5_HUMAN
26	43	55.1	297	1	YUBO_CAEEL
27	43	55.1	802	1	CIRB_RAT
28	43	55.1	806	1	CIRB_HUMAN
29	42	53.8	495	1	MURC_RICPR
30	41	52.6	769	1	SW16_KLUJA
31	40	51.3	616	1	CIR1_DROME
32	40	51.3	643	1	CIR4_DROME
33	40	51.3	656	1	CIR4_DROME

ALIGNMENTS

34	39	50.0	190	1	TEGU_SCHMA
35	39	50.0	266	1	IL1B_CEREL
36	39	50.0	556	1	YOF6_CAEEL
37	38	48.7	167	1	YXS5_CAEEL
38	38	48.7	293	1	BLAC_RHOCA
39	38	48.7	559	1	PAGT_HUMAN
40	38	48.7	559	1	PAGT_RAT
41	38	48.7	944	1	NUF1_YEAST
42	37	47.4	327	1	YGB7_ALCEU
43	37	47.4	399	1	MYC_CARAU
44	37	47.4	806	1	CIRB_CANFA
45	37	47.4	830	1	YDNI_SCHPO

RESULT 1
CIR2_MOUSE
ID CIR2_MOUSE STANDARD: PRT: 499 AA.
AC P15386; Q02010;
DT 01-APR-1990 (Rel. 14, Created)
DR 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.2 (RBK2) (RCK5) (NGK1) (MK2) (HUKIV).
GN KCNA2.
OS Mus musculus (Mouse), and Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-RAT;
RX MEDLINE=89255260; PubMed=2722779;
RA McKinnon D.;
RT "Isolation of a cDNA clone coding for a putative second potassium channel indicates the existence of a gene family."
RL J. Biol. Chem. 264:8230-8236(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-RAT; TISSUE=BRAIN;
RX MEDLINE=90059914; PubMed=2555158;
RA Stuehmer W., Ruppersberg J.P., Schroeter K.H., Sakmann B., Stocker M., Giese K.P., Perschke A., Baumann A., Pongs O.;
RT "Molecular basis of functional diversity of voltage-gated potassium channels in mammalian brain."
RL EMBO J. 8:3235-3244(1989).
RN [3]
RP REVISIONS.
RA Ludwig J.;
RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-RAT;
RX MEDLINE=91352097; PubMed=1715584;
RA Paulmichl M., Nasimith P., Herlitz R., Reed K., Boyle W.A., Paulmichl J.M., Peralta E.G., Clapham D.E.;
RT "Cloning and expression of a rat cardiac delayed rectifier potassium channel."
RL Proc. Natl. Acad. Sci. U.S.A. 88:7892-7895(1991).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES-MOUSE;
RX MEDLINE=90161996; PubMed=2305265;
RA Chandry K.G., Williams C.B., Spencer R.H., Aguilar B.A., Ghoshani S., Tempel B.L., Guitman G.A.;
RT "A family of three mouse potassium channel genes with intronless coding regions."
RL Science 247:973-975(1990).
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH

```
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J04731: AAA0819.1; -
DR EMBL: X16003: CAA34134.1; -
DR EMBL: W74449: AAA1867.1; -
DR EMBL: M30440: AAA39713.1; -
DR PIR: A33814: A33814.
DR PIR: S06709: S06709.
DR PIR: B40090: B40090.
DR HSSP: P03621: 21FN.
DR MCD: MGT:96659: KCNA2.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR003091; -.
DR PFAM: PF00520: Ion_trans; 1.
DR PRINTS: PR00169: KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KM Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 164 182 SEGMENT S1.
FT TRANSMEM 222 243 SEGMENT S2.
FT TRANSMEM 255 275 SEGMENT S3.
FT TRANSMEM 293 311 SEGMENT S4.
FT TRANSMEM 328 347 SEGMENT S5.
FT TRANSMEM 389 411 SEGMENT S6.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 449 449 PHOSPHORYLATION (BY CAPR)
FT CONFLICT 411 411 S -> F (IN REF. 4).
FT SEQUENCE 499 AA: 56700 MW: 1145768038DCBB CRC64:
SQ
Query Match 100.0%; Score 78; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FAEADERDSOPFSIP 15
Db 348 FAEADERDSOPFSIP 362
RESULT 2
CIRK2_XENLA STANDARD; PRT; 499 AA.
ID CIRK2_XENLA
AC P22739;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.2 (XSH2).
OS Xenopus laevis (African clawed frog).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Amphibia: Batrachia: Anura: Mesobatrachia: Pipridae: Pipridae;
OC Xenopodinae: Xenopus.
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE-91026051; Pubmed-2223094;
RA Rabera A.B.;
RT "A potassium channel gene is expressed at neural induction.";
RL Neuron 5:691-701(1990)
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M35664: AAA49933.1; -
DR PIR: JH0313: JH0313.
DR HSSP: P03621: 21FN.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR003091; -.
DR PFAM: PF00520: Ion_trans; 1.
DR PRINTS: PR00169: KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KM Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 164 182 SEGMENT S1.
FT TRANSMEM 222 243 SEGMENT S2.
FT TRANSMEM 255 275 SEGMENT S3.
FT TRANSMEM 293 311 SEGMENT S4.
FT TRANSMEM 328 347 SEGMENT S5.
FT TRANSMEM 389 411 SEGMENT S6.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 449 449 PHOSPHORYLATION (BY CAPR)
FT SEQUENCE 499 AA: 56701 MW: 1145768038DCBB CRC64:
SQ
Query Match 100.0%; Score 78; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FAEADERDSOPFSIP 15
Db 348 FAEADERDSOPFSIP 362
RESULT 3
CIRK2_HUMAN STANDARD; PRT; 499 AA.
ID CIRK2_HUMAN
AC P16389;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.2 (RBK2) (HBK5) (NGK1)
DE (MK2) (HUKIV).
GN KCNA2.
OS Homo sapiens (human).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
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CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Ramaswami M., Gautam M., Kamb A., Rudy B., Tanouye M.A.,
RT Mathew M.K.;
RT "Human potassium channel genes: molecular cloning and functional
RT expression.";
RL Mol. Cell. Neurosci. 1:214-223(1990).
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -I- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL, WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC -----
DR EMBL: L02752; AAA36141.1; -.
DR HSSP; P03621; 2IFN.
DR MIM; 176262; -.
DR INTERPRO; IPR000636; -.
DR INTERPRO; IPR003091; -.
DR PFM; PF00520; Ion_trans; 1.
DR PRINTS; PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT FT TRANSMEM 164 182 SEGMENT S1.
FT FT TRANSMEM 222 243 SEGMENT S2.
FT FT TRANSMEM 255 275 SEGMENT S3.
FT FT TRANSMEM 293 311 SEGMENT S4.
FT FT TRANSMEM 328 347 SEGMENT S5.
FT FT TRANSMEM 389 411 SEGMENT S6.
FT FT CARBOHYD 38 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT MOD_RES 449 449 PHOSPHORYLATION (BY CAPK)
FT FT
FT SEQUENCE 499 AA; 56716 MW; 4B03F1B46A826C39 CRC64;

Query Match 94.9%; Score 74; DB 1; Length 499;
Best Local Similarity 93.3%; Pred. No. 9.8e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEADERDSQFPSP 15
DB 348 FAEADERDSQFPSP 362

RESULT 4
ID C1K6_HUMAN STANDARD; PRT; 529 AA.
AC P17658;
DT 01-AUG-1990 (Rel. 15. Created)
DT 01-AUG-1990 (Rel. 15. Last sequence update)
DT 15-JUL-1998 (Rel. 36. Last annotation update)

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DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL6 (HBR2)..
GN KCAAB6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RC MEDLINE=902692208; Pubmed=2347305;
RA Gripe A., Schroeter K.H., Ruppersberg J.P., Stocker M., Drewes T.,
RA Bech S., Pongs O.;
RT "Cloning and expression of a human voltage-gated potassium channel. A
RT novel member of the RCK potassium channel family.";
RL EMO J. 9:1749-1756(1990).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONAL IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- MISCELLANEOUS: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC -----
CC EMBL, X17622; CAA35623.1; -.
CC DR PIR, S15057; S15057.
CC DR MIM, 176257; -.
CC DR INTERPRO, IPR000636; -.
CC DR INTERPRO, IPR003091; -.
CC DR PFM, PF00520; Ion_Trans; 1.
CC DR PRINTS, PF00169; KCHANNEL.
CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Glycoprotein; Multigene family; Phosphorylation.
CC FT TRANSMEM 175 193 SEGMENT S1.
CC FT TRANSMEM 263 284 SEGMENT S2.
CC FT TRANSMEM 296 316 SEGMENT S3.
CC FT TRANSMEM 340 360 SEGMENT S4.
CC FT TRANSMEM 376 396 SEGMENT S5.
CC FT TRANSMEM 437 457 SEGMENT S6.
CC FT MOD_RES 511 511 PHOSPHORYLATION (BY CAPK)
CC FT (PROBABLE).
CC SQ SEQUENCE 529 AA; 58728 MW; 587010A1F9CD69F CRC64;
Oy 1 FAEADERSQSPSP 15
Db 396 FAEADDDSLPSP 410
Query Match 78.2%; Score 61; DB 1; Length 529;
Best Local Similarity 80.0%; Pred.No. 0.0022;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
RESULT 5
ID C1K6_RAT STANDARD; PRT; 530 AA.
AC P17659; P19025;
DT 01-AUG-1990 (rel. 15, Created)
DT 01-AUG-1990 (rel. 15, Last sequence update)

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DT 15-JUL-1998 (Rel. 36, last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL.6 (RCK2) (KV2).
GN KCNA6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN CORTEX;
RX MEDLINE=90269208; PubMed=2347305;
RA Gruppe A., Schroeter K.H., Ruppberg J.P., Stocker M., Drewes T.,
RA Beckh S., Pongs O.;
RT "Cloning and expression of a human voltage-gated potassium channel. A
RT novel member of the RCK potassium channel family.";
RL EMBO J. 9:1749-1756(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=90297965; PubMed=2361015;
RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B.,
RA Folander K., Luneau C.J., Antanavage J., Oliva C., Buhrow S.A.,
RA Bennett C., Stein R.B., Kaczmarek L.M.;
RT "Cloning and expression of cDNA and genomic clones encoding three
RT delayed rectifier potassium channels in rat brain.";
RL Neuron 4:929-939(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=91130598; PubMed=1993474;
RA Kirsch G.E., Drewe J.A., Verma S., Brown A.M., Joho R.H.;
RT "Electrophysiological characterization of a new member of the RCK
RT family of rat brain K⁺ channels.";
RL FEBS Lett. 278:55-60(1991).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- MISCELLANEOUS: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X17621; CAA35622.1; -;
DR EMBL: M27159; AAA41499.1; ALT_SEQ.
DR PIR: JH0167;
DR PIR: S12786; S12786.
DR INTERPRO: IPR000636; -;
DR INTERPRO: IPR003091; -;
DR PFM: PF00520; Ion_trans; 1.
DR PRINTS: PR00169; KCHANNEL.
KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 175 193 SEGMENT S1.
FT TRANSMEM 264 285 SEGMENT S2.
FT TRANSMEM 297 317 SEGMENT S3.
FT TRANSMEM 341 361 SEGMENT S4.
FT TRANSMEM 377 397 SEGMENT S5.

FT TRANSMEM 438 458 SEGMENT S6.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 222 222 PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT MOD_RES 512 512 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 528 528 (PROBABLE).
FT MOD_RES 528 528 PHOSPHORYLATION (BY CAPK)
FT CONFLICT 241 241 (POTENTIAL).
FT CONFLICT 333 333 S -> L (IN REF. 3).
FT CONFLICT 333 333 R -> G (IN REF. 2).
SQ SEQUENCE 530 AA; 58883 MW; 30A9774B6C1DA5 CRC64;

Query Match 76.9%; Score 60; DB 1; Length 530;
Best Local Similarity 80.0%; Pred. No. 0.0033;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAEDERSOPSPSP 15
DB 397 FAEDVDSDSPSP 411

RESULT 6
CIRK2_RABIT STANDARD; PRT; 273 AA.
ID CIRK2_RABIT
AC 009081;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 15-JUL-1998 (Rel. 36, last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL.2 (KC22) (FRAGMENT).
GN KCNA2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RX MEDLINE=9212505; PubMed=1733291;
RA Desir G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,
RA Igarashi P.;
RT "Isolation of putative voltage-gated epithelial K⁺-channel isoforms
RT from rabbit kidney and LLC-PK1 cells.";
RL Am. J. Physiol. 262:F151-F157(1992).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROTRIMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN, LIVER, KIDNEY.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
DR INTERPRO: IPR000636; -;
DR PFM: PF00520; Ion_trans; 1.
KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 84 102 SEGMENT S1.
FT TRANSMEM 137 158 SEGMENT S2.
FT TRANSMEM 190 190 SEGMENT S3.
FT TRANSMEM 206 224 SEGMENT S4.
FT TRANSMEM 241 260 SEGMENT S5.
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 273 273
SQ SEQUENCE 273 AA; 31722 MW; 86EA846B2362F2C CRC64;

Query Match 71.8%; Score 56; DB 1; Length 273;
 Best Local Similarity 84.6%; Pred. No. 0.0083;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 FAEADERDSOFS 13
 ||| ||| ||| |||
 Db 261 FAEVDEPDSOFS 273

RESULT 7
 C1KB.DROME STANDARD; PRT: 924 AA.

AC P17970;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAB (SHAB11).
 GN SHAB OR SHAB11.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90239553; PubMed-2333511;
 RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "K+ current diversity is produced by an extended gene family
 conserved in Drosophila and mouse.";
 RT Science 248:599-603(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90245668; PubMed-2336395;
 RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "Shal, Shab, and Shaw: three genes encoding potassium channels in
 Drosophila.";
 RT Nucleic Acids Res. 18:2173-2174(1990).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
 IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M32659; AAA28896.1; -
 DR PIR: S15058; S15058.
 DR HSSP: P01551; IACX.
 DR FLYBASE: FBgn0003383; Shab.
 DR INTERPRO: IPR000636; -
 DR INTERPRO: IPR003091; -
 DR PFAM: PF00520; Ion_trans; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

Query Match 69.2%; Score 54; DB 1; Length 924;
 Best Local Similarity 66.7%; Pred. No. 0.073;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FAEADERDSOFSIP 15
 ||| ||| ||| ||| |||
 Db 597 FAEKDEKTFVSIIP 611

RESULT 8
 C1KL.HUMAN STANDARD; PRT: 495 AA.

AC Q09470;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1).
 GN KCNA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Ramaswami M., Gautam M., Kamb A., Rudy B., Tanouye M.A.,
 RA Mathew M.K.;
 RT "Human potassium channel genes: molecular cloning and functional
 expression.";
 RT Mol. Cell. Neurosci. 1:214-223(1990).
 RN [2]
 RP VARIANTS AEKK PHE-174; SER-239; ILE-249 AND ALA-408.
 RX MEDLINE-95144169; PubMed-7842011;
 RA Browne D.L., Gancher S.T., Nutt J.G., Brunt E.R.P., Smith E.A.,
 RA Kramer P., Litt M.;
 RT "Episodic ataxia/myokymia syndrome is associated with point mutations
 in the human potassium channel gene, KCNA1.";
 RT Nat. Genet. 8:136-140(1994).
 RN [3]
 RP VARIANTS AEKK ARG-177; ALA-226 AND ILE-404.
 RX MEDLINE-98260872; PubMed-9600245;
 RA Scheffer H., Brunt E.R.P., Mol G.J.J., van der Vlies P., Stulp R.P.,
 RA Verlind E., Mantel G., Aveyanov Y.N., Hofstra R.M.W., Buys C.H.C.M.;
 RT "Three novel KCNA1 mutations in episodic ataxia type I families.";
 RT Hum. Genet. 102:464-466(1998).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE

```

CC CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC CC
CC CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC CC EVERY THIRD POSITION.
CC CC -1- DISEASE: DEFECTS IN KCNA1 ARE THE CAUSE OF MYOKYMIA WITH PERIODIC
CC CC ATAXIA (AEKX) (PAROXYSMAL OR EPISODIC ATAXIA (EA)). A DISEASE
CC CC CHARACTERIZED BY CONTINUOUS MUSCLE MOVEMENT (MYOKYMIA) AND
CC CC PERIODIC ATAXIA.
CC CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL, L02750; AAA36139.1; -.
CC CC DR HSSP; P03621; 21FN.
CC CC MIM; 176260; -.
CC CC DR MIM; 160120; -.
CC CC DR INTERPRO; IPR000636; -.
CC CC DR INTERPRO; IPR003091; -.
CC CC DR PFAM; PF00520; Ion_trans; 1.
CC CC DR PRINTS; PR00169; KCHANNEL.
CC CC KW Glycoprotein; Multigene family; Ion transport; Voltage-gated channel;
CC CC TRANSMEM 168 186 SEGMENT S1 (BY SIMILARITY).
CC CC FT TRANSMEM 221 242 SEGMENT S2 (BY SIMILARITY).
CC CC FT TRANSMEM 254 274 SEGMENT S3 (BY SIMILARITY).
CC CC FT TRANSMEM 290 309 SEGMENT S4 (BY SIMILARITY).
CC CC FT TRANSMEM 326 345 SEGMENT S5 (BY SIMILARITY).
CC CC FT TRANSMEM 387 408 SEGMENT S6 (BY SIMILARITY).
CC CC FT CARBOHYD 207 207 N-LINKED (GLUCNA. . .) (POTENTIAL).
CC CC FT MOD_RES 322 322 PHOSPHORYLATION (BY CAPK)
CC CC FT (POTENTIAL).
CC CC FT MOD_RES 445 445 PHOSPHORYLATION (BY CAPK)
CC CC FT (POTENTIAL).
CC CC FT MOD_RES 174 174 V -> F (IN AEKX).
CC CC FT VARIANT 174 174 /FTID-VAR_001508.
CC CC FT VARIANT 177 177 I -> R (IN AEKX).
CC CC FT VARIANT 226 226 /FTID-VAR_001509.
CC CC FT VARIANT 226 226 T -> A (IN AEKX).
CC CC FT VARIANT 239 239 /FTID-VAR_001510.
CC CC FT VARIANT 239 239 R -> S (IN AEKX).
CC CC FT VARIANT 249 249 /FTID-VAR_001511.
CC CC FT VARIANT 249 249 F -> I (IN AEKX).
CC CC FT VARIANT 404 404 /FTID-VAR_001512.
CC CC FT VARIANT 404 404 V -> I (IN AEKX).
CC CC FT VARIANT 408 408 /FTID-VAR_001513.
CC CC FT VARIANT 408 408 V -> A (IN AEKX).
CC CC FT VARIANT 408 408 /FTID-VAR_001514.
CC CC FT SO SEQUENCE 495 AA; 56541 MW; 0A1B1AB0536F5CBA CRC64;
CC CC
CC CC Query Match 65.4%; Score 51; DB 1; Length 495;
CC CC Best Local Similarity 66.7%; Pred. No. 0.13;
CC CC Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
CC CC
CC CC Oy 1 FAEADERDQSPSP 15
CC CC |||||:|:|:|:|
CC CC Db 346 PAFAEEAEASHSPSP 360
CC CC
CC CC RESULT 9
CC CC CIK1_MOUSE STANDARD; PRT; 495 AA.
CC CC AC P16388.
CC CC DT 01-AUG-1990 (rel. 15, Created)

```

DT	01-AUG-1990 (Rel. 15, Last sequence update)
DE	15-JUL-1998 (Rel. 36, Last annotation update)
GN	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (MK1) (MBK1).
OS	KCNAL.
OC	Mus musculus (Mouse).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
RA	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=9016196; PubMed=2305265;
RA	Chandy K.G., Williams C.B., Spencer R.H., Aguilar B.A.,
RT	Ghanshani S., Tempel B.L., Gutman G.A.;
RL	"A family of three mouse potassium channel genes with intronless coding regions".
SC	Science 247:973-975(1990).
LN	[2]
RN	SEQUENCE FROM N.A.
RC	TISSUE=BRAIN;
RX	MEDLINE=88189348; PubMed=2451788;
RA	Tempel B.L., Jan Y.N., Jan L.Y.;
RL	"Cloning of a probable potassium channel gene from mouse brain.";
Nature 333:837-839(1988).	
CC	-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
CC	-1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	-1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE RATE OF INACTIVATION OF THE CHANNEL, WHILE THE TAIL MAY PLAY A ROLE IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC	-1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC	-1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC	-----
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CC	-----
DR	EMBL; M30439; AAA39711.1; -;
DR	EMBL; Y00305; CAAG8408.1; -;
DR	PIR; S06378; S06378.
DR	PIR; A40090; A40090.
DR	HSSP; P03621; ZIFN.
DR	MGP; MG1:96654; KCNAL.
DR	INTERPRO; IPRO00636; -;
DR	INTERPRO; IPRO03091; -;
DR	Pfam; PF00520; Ion_trans; 1.
DR	PRINTS; PR00169; KCNALNL.
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW	Glycoprotein; Multigene family; Phosphorylation.
KW	TRANSMEM 168 186 SEGMENT S1.
FT	TRANSMEM 221 242 SEGMENT S2.
FT	TRANSMEM 254 274 SEGMENT S3.
FT	TRANSMEM 290 309 SEGMENT S4.
FT	TRANSMEM 326 345 SEGMENT S5.
FT	TRANSMEM 387 408 SEGMENT S6.
FT	CARBOHD 207 207 N-LINKED (GLNCAC. .) (POTENTIAL).
FT	MOD_RES 322 322 PHOSPHORYLATION (BY CAPK (POTENTIAL)).
FT	MOD_RES 446 446 PHOSPHORYLATION (BY CAPK (POTENTIAL)).
FT	MOD_RES 495 AA; 56409 MW; C9249F130E9A3D3D CRC64;
SE	SEQUENCE


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CC or send an email to license@sdb.sdb.ch).
CC -----
DR EMBL; X16476; CAA34497.1; -.
DR PIR; S05448; CHRTL1.
DR INTERPRO; IPR000636; -.
DR INTERPRO; IPR003091; -.
DR PFAM; PF00520; Ion.trans; 1.
DR PRINTS; PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KM Glycoprotein; Multigene family; Phosphorylation.
FT DOMAIN 1 182 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 183 204 SEGMENT S1 (POTENTIAL).
FT DOMAIN 205 224 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 225 246 SEGMENT S2 (POTENTIAL).
FT DOMAIN 247 256 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 257 278 SEGMENT S3 (POTENTIAL).
FT DOMAIN 279 290 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 291 312 SEGMENT S4 (POTENTIAL).
FT DOMAIN 313 326 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 327 348 SEGMENT S5 (POTENTIAL).
FT DOMAIN 349 388 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 389 410 SEGMENT S6 (POTENTIAL).
FT DOMAIN 411 853 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 440 440 PHOSPHORYLATION (BY CAPK (POTENTIAL)).
FT MOD_RES 492 492 PHOSPHORYLATION (BY CAPK (POTENTIAL)).
SQ SEQUENCE 853 AA; 95280 MW; 7A0899839716165 CRC64;
Query Match 65.4%; Score 51; DB 1; Length 853;
Best Local Similarity 66.7%; Pred. No. 0.23;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 1 FAEDERDSDPESP 15
   ||| ||| ||| |||
Db 347 FAEKDEDDTKERSIP 361

RESULT 12
C1KA_HUMAN STANDARD; PRT; 854 AA.
AC Q14721;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DHK1).
GN KCNB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Ikeda S.R., Soler F., Zuhke R.D., Joho R.H., Lewis D.L.;
RL Submitted (JAN-1993) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER

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CC CLASS: BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL, L02840; AAA36156.1; -.
CC DR MIM: 600397; -.
CC DR INTERPRO: IPR000636; -.
CC DR INTERPRO: IPR003091; -.
CC DR PFM: PFM00520; Ion.trans: 1.
CC DR PRINTS: PR00169; KCHANNEL.
CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Glycoprotein; Multigene family;
CC FT DOMAIN 1 182
CC FT TRANSMEM 183 204 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 205 224 SEGMENT S1 (POTENTIAL).
CC FT TRANSMEM 225 246 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 247 256 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 257 278 SEGMENT S3 (POTENTIAL).
CC FT DOMAIN 279 290 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 291 312 SEGMENT S4 (POTENTIAL).
CC FT DOMAIN 313 326 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 327 348 SEGMENT S5 (POTENTIAL).
CC FT DOMAIN 349 388 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 389 410 SEGMENT S6 (POTENTIAL).
CC FT DOMAIN 411 834 CYTOPLASMIC (POTENTIAL).
CC FT MOD_RES 440 440 PHOSPHORYLATION (BY CAPK)
CC FT MOD_RES 440 440 PHOSPHORYLATION (BY CAPK)
CC FT MOD_RES 492 492 PHOSPHORYLATION (BY CAPK)
CC FT MOD_RES 492 492 PHOSPHORYLATION (BY CAPK)
CC FT CARBOHYD 279 279 N-LINKED (GLCNAC... ) (POTENTIAL).
CC FT SEQUENCE 854 AA; 95521 MW; 360DBE3E45731EDA CMC64;
CC
CC Query Match 65.4%; Score 51; DB 1; Length 854;
CC Best Local Similarity 66.7%; Pred. No. 0.23;
CC Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 1 FAADERDQFPSP 15
CC I I I I I I I I I I
CC Db 347 FAEKDEDDTKRKSIP 361
CC
CC RESULT 13
CC CIRS_MUSPF STANDARD: PRT: 601 AA.
CC AC P79197;
CC DT 30-MAY-2000 (Rel. 39, Created)
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL.5.
CC GN KCNMA5.
CC OS Mustela putorius furo (Ferret).
CC OC Eukaryota; Metazoa; Chordata; Granata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=HEART ATRIUM;
CC RA Schweigel T., Folander K., Swanson R.;
CC RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
CC CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT (BY SIMILARITY).
CC CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS

```

CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
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 CC -----
 CC EMBL: U45979; AAB41145.1; -
 CC INTERPRO: IPR000636; -
 CC DR PFAM: PF00520; Ion_trans. 1.
 CC DR PRINTS: PR00169; KCHANNEL.
 CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycoprotein; Multigene family; Phosphorylation.
 CC FT TRANSMEM 240 258 SEGMENT S1.
 CC FT TRANSMEM 314 334 SEGMENT S2.
 CC FT TRANSMEM 345 366 SEGMENT S3.
 CC FT TRANSMEM 386 407 SEGMENT S4.
 CC FT TRANSMEM 422 443 SEGMENT S5.
 CC FT TRANSMEM 483 504 SEGMENT S6.
 CC FT DOMAIN 370 375 POLY-GLY
 CC FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SQ SEQUENCE 601 AA; 65889 MW; 142DB9F8CB8A3FE0 CRC64;
 CC
 CC Query Match 62.8%; Score 49; DB 1; Length 601;
 CC Best Local Similarity 60.0%; Pred. No. 0.35;
 CC Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 CC
 CC OY 1 FAEADERSOFPSP 15
 CC Db 442 FAEADNGETHFSIP 456
 CC
 CC RESULT 14
 CC CIK5_MOUSE STANDARD; PRT; 602 AA.
 CC AC Q61762;
 CC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
 CC DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.5 (KVL1-5).
 CC GN KCNA5.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-SWISS: TISSUE=HEART;
 CC RX MEDLINE=94043264; PubMed=8226976;
 CC RA Altai B., Lesage F., Ziliati P., Guilleme E., Honore E.,
 CC RA Walman R., Hugnot J.-P., Mattei M.-G., Lazdunski M., Barhanin J.;
 CC RT "Multiple mRNA isoforms encoding the mouse cardiac Kvl-5 delayed
 CC RT rectifier K+ channel."
 CC RL J. Biol. Chem. 268:24283-24289(1993).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; KVL1-5 (SHOWN HERE), KVL1-5/5/
 CC AND KVL1-5/3'; ARE PRODUCED BY ALTERNATIVE SPLICING. KVL1-5/3' IS
 CC NON-FUNCTIONAL BUT INHIBITS EXPRESSION OF KVL1-5.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART AND MODERATELY
 CC IN BRAIN. LOW LEVELS IN THYMUS, SKELETAL MUSCLE AND SPLEEN. NOT
 CC EXPRESSED IN LIVER, LUNG OR KIDNEY.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
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 CC -----
 CC EMBL: L22218; AAA39365.1; -
 CC HSSP: P03621; 2IFN.
 CC DR MGI: 96662; KCNA5.
 CC DR INTERPRO: IPR000636; -
 CC DR INTERPRO: IPR003091; -
 CC DR PFAM: PF00520; Ion_trans. 1.
 CC DR PRINTS: PR00169; KCHANNEL.
 CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycoprotein; Multigene family; Phosphorylation;
 CC Alternative splicing.
 CC FT TRANSMEM 242 260 SEGMENT S1.
 CC FT TRANSMEM 316 336 SEGMENT S2.
 CC FT TRANSMEM 347 368 SEGMENT S3.
 CC FT TRANSMEM 387 408 SEGMENT S4.
 CC FT TRANSMEM 423 444 SEGMENT S5.
 CC FT TRANSMEM 484 505 SEGMENT S6.
 CC FT DOMAIN 373 376 POLY-GLY
 CC FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT MOD_RES 81 81 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 CC FT MOD_RES 81 81 PHOSPHORYLATION (BY CK2) (POTENTIAL).
 CC FT MOD_RES 535 535 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 CC FT MOD_RES 546 546 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 CC FT MOD_RES 569 569 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 CC FT VARSPPLIC 1 200 MISSING (IN ISOFORM KVL1-5/3').
 CC FT VARSPPLIC 515 602 MISSING (IN ISOFORM KVL1-5/3').
 CC SQ SEQUENCE 602 AA; 66644 MW; FC2092B8062FAC97 CRC64;
 CC
 CC Query Match 61.5%; Score 48; DB 1; Length 602;
 CC Best Local Similarity 66.7%; Pred. No. 0.54;
 CC Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC OY 1 FAEADERSOFPSP 15
 CC Db 443 FAEADNQSOLSSIP 457
 CC
 CC RESULT 15
 CC CIK5_RAT STANDARD; PRT; 602 AA.
 CC ID CIK5_RAT
 CC AC P19024;
 CC DT 01-NOV-1990 (Rel. 16, Created)
 CC DT 01-NOV-1990 (Rel. 16, Last sequence update)
 CC DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (KV1) (RCK7).
GN KCNA5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA MEDLINE-90297965; PubMed-2361015;
RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B.,
RA Follender K., Luneau C.J., Antanavage J., Oliva C., Bubrow S.A.,
RA Bennett C., Stein R.B., Kaczmarek L.M.;
RT "Cloning and expression of cDNA and genomic clones encoding three
RT delayed rectifier potassium channels in rat brain.";
RL Neuron 4:929-939(1990).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC -----
DR EMBL; M27158; AAA1498.1; -;
DR PIR; JH0166; JH0166.
DR HSSP; P03621; 21FN.
DR INTERPRO; IPR000636; -;
DR INTERPRO; IPR003091; -;
DR PFAM; PF00520; Ion.trans.1.
DR PRINTS; PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 242 260 SEGMENT S1.
FT TRANSMEM 316 336 SEGMENT S2.
FT TRANSMEM 347 368 SEGMENT S3.
FT TRANSMEM 387 408 SEGMENT S4.
FT TRANSMEM 423 444 SEGMENT S5.
FT TRANSMEM 484 505 SEGMENT S6.
FT DOMAIN 373 376 POLY-GLY.
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 81 81 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 81 81 PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT MOD_RES 535 535 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 546 546 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 569 569 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
SQ SEQUENCE 602 AA; 66552 MW; 6A784535FF226ED7 CRC64;

Oy 1 FAEADERSQPSIP 15
||||| | | | |
Db 443 FAEADNHSHPSSIP 457

Search completed: February 2, 2001, 10:41:47
Job time: 311 sec

Query Match 61.5%; Score 48; DB 1; Length 602;
Best Local Similarity 66.7%; Pred. No. 0.54;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: February 2, 2001, 10:35:47 ; Search time 38.22 Seconds
(without alignments)
26.649 Million cell updates/sec

Title: US-09-273-217-1
Perfect score: 78
Sequence: 1 FAEADERDSQFPSP 15

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues
Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	57	2 S09046	potassium channel
2	78	100.0	476	2 S21144	potassium channel
3	78	100.0	499	2 JH0313	potassium channel
4	78	100.0	499	2 I84204	potassium channel
5	78	100.0	499	2 A33814	potassium channel
6	74	94.9	499	2 I77466	potassium channel
7	74	94.9	499	2 A48672	potassium channel
8	67	89.9	266	2 I46855	delayed rectifier
9	61	78.2	529	2 S12787	voltage-gated pota
10	60	76.9	57	2 S09043	potassium channel
11	60	76.9	530	2 JH0167	potassium channel
12	54	69.2	924	2 B41359	potassium channel
13	54	69.2	924	2 S12746	potassium channel
14	51	65.4	57	2 S09042	potassium channel
15	51	65.4	495	2 I57680	potassium channel
16	51	65.4	495	2 A40090	potassium channel
17	51	65.4	495	2 B39113	potassium channel
18	51	65.4	853	1 CHRTD1	potassium channel
19	51	65.4	857	2 I36529	potassium channel
20	51	65.4	858	2 S13761	potassium channel
21	50	64.1	489	2 I51532	potassium channel
22	49	62.8	49	2 S09049	potassium channel
23	49	62.8	482	2 T15829	hypothetical prote
24	48	61.5	514	2 C48507	potassium channel
25	48	61.5	602	2 A43507	potassium channel
26	48	61.5	602	2 JH0166	potassium voltage-
27	48	61.5	653	2 A39922	potassium channel
28	48	61.5	654	2 S11049	potassium channel
29	48	61.5	654	2 E39113	potassium channel

30	48	61.5	660	2 S24125	potassium channel
31	46	59.0	57	2 S09044	potassium channel
32	46	59.0	57	2 S09047	potassium channel
33	46	59.0	523	2 A38101	potassium channel
34	46	59.0	523	2 I52990	voltage-gated pota
35	46	59.0	525	2 A43531	potassium channel
36	46	59.0	528	2 I84205	potassium channel
37	46	59.0	598	2 S66659	potassium channel
38	46	59.0	613	2 A56031	potassium channel
39	45	57.7	57	2 S09048	potassium channel
40	45	57.7	57	2 S09045	potassium channel
41	45	57.7	597	2 S51212	BAK5 protein - bov
42	43	55.1	297	2 T21387	hypothetical prote
43	43	55.1	802	2 JH0595	potassium channel
44	42	53.8	460	2 T27759	hypothetical prote
45	42	53.8	495	2 C71679	UDP-n-acetylurama

ALIGNMENTS

RESULT 1
S09046
potassium channel protein MK-5 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence-revision 30-Sep-1991 #text-change 18-Jun-1993
C:Accession: S09046
R:Betsholtz, C.; Baumann, A.; Kenna, S.; Ashcroft, F.M.; Ashcroft, S.J.H.; Berggren,
FEBS Lett. 263, 121-126, 1990
A:Title: Expression of voltage-gated K⁺ channels in insulin-producing cells. Analysis
A:Reference number: S09042; MUID:90235950
A:Accession: S09046
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-57 <BET>

Query Match 100.0%; Score 78; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAEADERDSQFPSP 15
DB 11 FAEADERDSQFPSP 25

RESULT 2
S21144
potassium channel protein RCK5 - bovine (fragment)
N:Alternate names: potassium channel protein 2
C:Species: Bos primigenius taurus (cattle)
C:Date: 22-Nov-1993 #sequence-revision 05-Apr-1995 #text-change 05-Nov-1999
C:Accession: S21144; A23668; A33158
R:Reid, P.F.; Pongs, O.; Dolly, J.O.
FEBS Lett. 302, 31-34, 1992.
A:Title: Cloning of a bovine voltage-gated K(+) channel gene utilising partial amino
A:Reference number: S21144; MUID:92267180
A:Accession: S21144
A:Molecule type: DNA
A:Residues: 1-476 <RET>
A:Cross-references: GR:X66185; NID:9395206; PTDN:CA46953.1; PTD:9395207
A>Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 320-
R:Scott, V.E.S.; Parcej, D.N.; Keen, J.N.; Findlay, J.B.C.; Dolly, J.O.
J. Biol. Chem. 269, 20094-20097, 1990
A:Title: alpha-bendroloxin acceptor from bovine brain is a K(+) channel protein. Evid
A:Reference number: A23668; MUID:91056043
A:Accession: A23668
A:Molecule type: protein
A:Residues: 2-28 <SC0>
R:Newitt, R.A.; Houamed, K.M.; Rehm, H.; Tempel, B.L.
submitted to the Protein Sequence Database, February 1991
A:Reference number: A33158
A:Accession: A33158

A:Molecule type: protein
A:Residues: 2-27 <NEW>
C:Accession: A33814; C39113; S06709; I59204
C:Keywords: glycoprotein; transmembrane protein
F:38,207/466/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 78; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEADERSQPSIP 15
|||||
DB 348 FAEADERSQPSIP 362

RESULT 3
JH0313
potassium channel protein Xsha2 - African clawed frog

C:Species: Xenopus laevis (African clawed frog)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: JH0313
R:Ribera, A.B.
Neuron 5, 691-701, 1990
A:Title: A potassium channel gene is expressed at neural induction.
A:Reference number: JH0313; MUID:91026051

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-499 <RTB>

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEADERSQPSIP 15
|||||
DB 348 FAEADERSQPSIP 362

RESULT 4
I84204
potassium channel protein MK2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: B40090; I84204
R:Chandy, K.G.; Williams, C.B.; Spencer, R.H.; Aguilar, B.A.; Ghanashani, S.; Tempel, B.L.
Science 247, 973-975, 1990
A:Title: A family of three mouse potassium channel genes with intronless coding regions.
A:Reference number: A40090; MUID:90161996
A:Accession: B40090
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-499 <CHA>
A:Cross-references: GB:M30440; NID:q199706; PIDN:AAA39713.1; PID:q199707
C:Genetics:
A:Gene: MK2

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEADERSQPSIP 15
|||||
DB 348 FAEADERSQPSIP 362

RESULT 5
A33814
potassium channel KVL2 - rat
N:Alternate names: potassium channel RCK5; potassium channel RK2; RAK
C:Species: Rattus norvegicus (Norway rat)

C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 05-Nov-1999
C:Accession: A33814; C39113; S06709; I59204
R:McKinnon, D.
J. Biol. Chem. 264, 8230-8236, 1989

A:Title: Isolation of a cDNA clone coding for a putative second potassium channel ind
A:Reference number: A33814; MUID:89255260
A:Accession: A33814
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-499 <MCK>

A:Cross-references: GB:J04731; NID:q203154; PIDN:AAA40819.1; PID:q203155
R:Roberts, S.L.; Tankun, M.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991

A:Title: Cloning and tissue-specific expression of five voltage-gated potassium chann
A:Reference number: A39113; MUID:91156694
A:Accession: C39113
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: mRNA
A:Residues: 1-12,24-499 <ROB>
R:Stuehmer, W.; Ruppersberg, J.P.; Schroeter, K.H.; Sakmann, B.; Giese, E.
EMBO J. 8, 3235-3244, 1989

A:Title: Molecular basis of functional diversity of voltage-gated potassium channels
A:Reference number: S06708; MUID:90059914
A:Accession: S06709
A:Molecule type: mRNA

A:Residues: 1-247, 'SC', 250-261, 'T', 263-282, 'HTNR', 288-291, 'T', 293-499 <STU>
A:Cross-references: EMBL:X16003
R:Paumlich, M.; Nasmitz, P.; Herlitz, R.; Reed, K.E.; Boyle, W.A.; Nerbonne, J.M.;
Proc. Natl. Acad. Sci. U.S.A. 88, 7892-7895, 1991

A:Title: Cloning and expression of a rat cardiac delayed rectifier potassium channel.
A:Reference number: I59204; MUID:91352097
A:Accession: I59204
A:Status: preliminary; translated from GB/EMBL/DDB

A:Molecule type: mRNA
A:Residues: 1-410, 'F', 412-499 <RES>
A:Cross-references: GB:M74449; NID:q206548; PIDN:AAA19867.1; PID:q206549
A:Experimental source: heart atrium
C:Genetics:
A:Gene: RAK

C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane
F:164-182/Domain: transmembrane #status predicted <TM1>
F:222-243/Domain: transmembrane #status predicted <TM2>
F:253-273/Domain: transmembrane #status predicted <TM3>
F:288-311/Domain: transmembrane #status predicted <TM4>
F:328-347/Domain: transmembrane #status predicted <TM5>
F:363-372/Domain: transmembrane beta strand #status predicted <TM6>
F:373-381/Domain: transmembrane beta strand #status predicted <TM7>
F:389-411/Domain: transmembrane #status predicted <TM8>
F:207/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:449/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEADERSQPSIP 15
|||||
DB 348 FAEADERSQPSIP 362

RESULT 6
I77466

potassium channel - human
C:Species: Homo sapiens (man)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I77466
R:Ramashwami, M.; Gautam, M.; Kamb, A.A.; Rudy, B.; Tanoye, M.A.; Mathew, M.K.
Mol. Cell. Neurosci. 1, 214-223, 1990

A:Title: Human potassium channel genes: molecular cloning and functional expression.
A:Reference number: I57680
A:Accession: I77466

A:Status: preliminary; translated from GB/EMBL/DDB

A:Molecule type: mRNA
 A:Residues: 1-499 <RES>
 A:Cross-references: GB:L02752; NID:9186668; PIDN:AAA36141.1; PID:9186669

Query Match
 Best Local Similarity 93.3%; Score 74; DB 2; Length 499;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEADERDSQFSPSIP 15
 |||||||:|||||||
 Db 348 FAEADERESQFSPSIP 362

RESULT 7
 A48672
 delayed rectifier potassium channel Kv1.2, smooth muscle - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
 C:Accession: A48672
 R:Hart, P.J.; Overlurf, K.E.; Russell, S.N.; Carl, A.; Hume, J.R.; Sanders, K.M.; Horowitz, Natl. Acad. Sci. U.S.A. 90, 9659-9663, 1993
 A:Title: Cloning and expression of a K-v1.2 class delayed rectifier K(+) channel from ca
 A:Reference number: A48672; MUID:94022435
 A:Accession: A48672
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-499 <HAR>
 A:Cross-references: GB:L19740; NID:9304651; PIDN:AAA03607.1; PID:9304652
 A:Keywords: smooth muscle

Query Match
 Best Local Similarity 94.9%; Score 74; DB 2; Length 499;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEADERDSQFSPSIP 15
 |||||||:|||||||
 Db 348 FAEADERESQFSPSIP 362

RESULT 8
 I46855
 voltage-gated potassium channel - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
 C:Accession: I46855
 R:Desir, G.; Velazquez, H.
 Am. J. Physiol. 264, 128-133, 1993
 A:Title: Identification of a novel K-channel gene (KC22) that is highly expressed in dis
 A:Reference number: I46855
 A:Accession: I46855
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-286 <DES>
 A:Cross-references: GB:L01789; NID:9165448; PIDN:AAA1380.1; PID:9165449

Query Match
 Best Local Similarity 85.9%; Score 67; DB 2; Length 286;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEADERDSQFSPS 13
 |||||||:|||||||
 Db 274 FAEADERDSQFSPS 286

RESULT 9
 S12787
 potassium channel KCNA2 - human
 N:Alternate names: potassium channel HBK2
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999

C:Accession: S12787; S15057
 R:Grube, A.; Schroeter, K.H.; Ruppersberg, J.P.; Stocker, M.; Drewes, T.; Beckh, S.; EMO J. 9, 1749-1756, 1990
 A:Title: Cloning and expression of a human voltage-gated potassium channel. A novel m
 A:Reference number: S12786; MUID:90269208
 A:Accession: S12787

A:Molecule type: mRNA
 A:Residues: 1-529 <GRU>
 A:Cross-references: EMBL:X17622
 R:Pongs, O.
 submitted to the EMBL Data Library, November 1989
 A:Reference number: S15057
 A:Accession: S15057

A:Molecule type: mRNA
 A:Residues: 1-57, 59-529 <PON>
 A:Cross-references: EMBL:X17622; NID:932032; PIDN:CAA35623.1; PID:932033
 C:Genetics:
 A:Gene: GDB:KCNA2; HK4; KV1.2
 A:Cross-references: GDB:128062; OMIM:176262
 C:Keywords: glycoprotein; ion channel; transmembrane protein
 F:175-193/Domain: transmembrane #status predicted <TM1>
 F:263-284/Domain: transmembrane #status predicted <TM2>
 F:296-316/Domain: transmembrane #status predicted <TM3>
 F:340-359/Domain: transmembrane #status predicted <TM4>
 F:376-395/Domain: transmembrane #status predicted <TM5>
 F:437-458/Domain: transmembrane #status predicted <TM6>

Query Match
 Best Local Similarity 78.2%; Score 61; DB 2; Length 529;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FAEADERDSQFSPSIP 15
 |||||:|||||||
 Db 396 FAEADDDSLFSPSIP 410

RESULT 10
 S09043
 potassium channel protein MK-2 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
 C:Accession: S09043
 R:Bertholz, C.; Baumann, A.; Kenna, S.; Ashcroft, F.M.; Ashcroft, S.J.H.; Berggren, FEBS Lett. 263, 121-126, 1990
 A:Title: Expression of voltage-gated K⁺ channels in insulin-producing cells. Analysis
 A:Reference number: S09042; MUID:90235950
 A:Accession: S09043
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-57 <BET>

Query Match
 Best Local Similarity 76.9%; Score 60; DB 2; Length 57;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FAEADERDSQFSPSIP 15
 |||||:|||||||
 Db 11 FAEADVDLSPSIP 25

RESULT 11
 JH0167
 potassium channel Kv1.6 - rat
 N:Alternate names: potassium channel Kv2; potassium channel RCK2
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 05-Nov-1999
 C:Accession: JH0167; S12786
 R:Swanson, R.; Marshall, J.; Smith, J.S.; Williams, J.B.; Boyle, M.B.; Polander, K.; Neuron 4, 929-939, 1990
 A:Title: Cloning and expression of cDNA and genomic clones encoding three delayed rec
 A:Reference number: JH0166; MUID:90297965

A:Accession: JH0167
A:Molecule type: mRNA
A:Residues: 1-530 <SWA>
A:Cross-references: GB:M27159
A:Experimental source: Brain
R:Gruppe, A.; Schroeter, K.H.; Ruppersberg, J.P.; Stocker, M.; Drewes, T.; Beckh, S.; Port
EMBO J. 9, 1749-1756, 1990
A:Title: Cloning and expression of a human voltage-gated potassium channel. A novel mem
A:Reference number: S12786; MUID:90269208
A:Accession: S12786
A:Molecule type: mRNA
A:Residues: 1-332, 'R', 334-530 <GRU>
A:Cross-references: EMBL:X17621; NID:957666; PIDN:CAA35622.1; PID:957667
C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane bet
F:175-193/Domain: transmembrane #status predicted <TM1>
F:264-285/Domain: transmembrane #status predicted <TM2>
F:297-317/Domain: transmembrane #status predicted <TM3>
F:341-360/Domain: transmembrane #status predicted <TM4>
F:377-396/Domain: transmembrane #status predicted <TM5>
F:412-421/Domain: transmembrane beta strand #status predicted <TMB1>
F:422-430/Domain: transmembrane beta strand #status predicted <TMB2>
F:438-459/Domain: transmembrane #status predicted <TM6>
F:512/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic
F:528/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predic

Query Match 76.9%; Score 60; DB 2; Length 530;
Best Local Similarity 80.0%; Pred. No. 0.0063;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 FAEADERDQFPSP 15
|||||: || |||||
Db 397 FAEADVDVSLPSP 411

RESULT 12
B41359
potassium channel protein shab11 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 16-Feb-1997
C:Accession: B41359
R:Butler, A.; Wei, A.; Baker, K.; Salkoff, L.
Science 243, 943-947, 1989
A:Title: A family of putative potassium channel genes in Drosophila.
A:Reference number: A41359; MUID:89146139
A:Accession: B41359
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-924 <BUT>
A:Cross-references: GB:M32659
C:Genetics:
A:Gene: FlyBase:Shab
A:Cross-references: FlyBase:FBgn0003383
C:Superfamily: potassium channel protein drk1

Query Match 69.2%; Score 54; DB 2; Length 924;
Best Local Similarity 66.7%; Pred. No. 0.14;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY 1 FAEADERDQFPSP 15
|||||: || |||||
Db 597 FAEKDKTKFVSP 611

RESULT 13
S12746
potassium channel protein shab11 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Aug-1999
C:Accession: S12746; S15058
R:Butler, A.; Wei, A.; Salkoff, L.
Nucleic Acids Res. 18, 2173-2174, 1990

A:Title: Shal, Shab, and Shaw: three genes encoding potassium channels in Drosophila.
A:Reference number: S12746; MUID:90245668
A:Accession: S12746
A:Molecule type: mRNA
A:Residues: 1-924 <BUT>
A:Cross-references: EMBL:M32659
R:Butler, A.; Wei, A.; Salkoff, L.
submitted to the EMBL Data Library, March 1990
A:Description: Shal, Shab, and Shaw: Three genes encoding potassium channels in Droso
A:Reference number: S15058
A:Accession: S15058
A:Molecule type: mRNA
A:Residues: 1-625, 'Y', 628-924 <BUT>
A:Cross-references: EMBL:M32659; NID:9158458; PIDN:AA28896.1; PID:9158459
C:Genetics:
A:Gene: shab11
A:Cross-references: FlyBase:FBgn0003383
C:Superfamily: potassium channel protein drk1
C:Keywords: ion channel; potassium channel; transmembrane protein

Query Match 69.2%; Score 54; DB 2; Length 924;
Best Local Similarity 66.7%; Pred. No. 0.14;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY 1 FAEADERDQFPSP 15
|||||: || |||||
Db 597 FAEKDKTKFVSP 611

RESULT 14
S09042
potassium channel protein MK-1 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C:Accession: S09042
R:Bertholtz, C.; Baumann, A.; Kenna, S.; Ashcroft, F.M.; Ashcroft, S.J.H.; Berggren,
FEBS Lett. 263, 121-126, 1990
A:Title: Expression of voltage-gated K⁺ channels in insulin-producing cells. Analysis
A:Reference number: S09042; MUID:90235950
A:Accession: S09042
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-57 <BET>

Query Match 65.4%; Score 51; DB 2; Length 57;
Best Local Similarity 66.7%; Pred. No. 0.022;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 1 FAEADERDQFPSP 15
|||||: || |||||
Db 11 FAEAEAFHSFSP 25

RESULT 15
I57680
potassium channel KCNA1 - human
N:Alternate names: potassium channel protein HKC-1
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 08-Oct-1999
C:Accession: I57680; A60173
R:Ramashwami, M.; Gautam, M.; Kamp, A.A.; Rudy, B.; Tanouye, M.A.; Mathew, M.K.
Mol. Cell. Neurosci. 1, 214-223, 1990
A:Title: Human potassium channel genes: molecular cloning and functional expression.
A:Reference number: I57680
A:Accession: I57680
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-495 <RAM>
A:Cross-references: GB:I02750; NID:g186662; PIDN:AAA36139.1; PID:g186663
R:Freeman, S.N.; Conley, E.C.; Brennand, J.C.; Russell, N.J.W.; Brammar, W.J.
Biochem. Soc. Trans. 18, 891a, 1990

A:Title: Cloning and characterization of a cDNA encoding a human brain potassium channel
A:Reference number: A60173; MUID:91192386
A:Accession: A60173
A:Molecule type: mRNA
A:Residues: 263-264,266-314,'R' <FRE>
C:Genetics:
A:Gene: GDB:KCNAL; RBK1; HUK1; MBK1; AEMK; KVL.1
A:Cross-references: GDB:127903; OMIM:176260
A:Map position: 12p13-12p13

Query Match 65.4%; Score 51; DB 2; Length 495;
Best Local Similarity 66.7%; Pred. No. 0.24;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 FAADERDSQFPSIP 15
||||:|:| | |||
DB 346 FAAEAEESHFSIP 360

Search completed: February 2, 2001, 10:37:10
Job time: 83 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 2, 2001, 10:35:47 ; Search time 34.98 Seconds
(without alignments)
7.700 Million cell updates/sec

Title: US-09-273-217-1

Perfect score: 78
Sequence: 1 FAEDERDSQFSPSP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing First 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	65.4	539	1	US-08-464-340A-13
2	46	59.0	528	2	US-08-527-152-2
3	45	57.7	532	1	US-08-288-405A-10
4	36.5	46.8	1121	1	US-07-789-915A-2
5	36.5	46.8	1121	1	US-08-005-002C-2
6	36.5	46.8	1121	1	US-08-087-203A-2
7	36.5	46.8	1134	5	5476657-1
8	36.5	46.8	1403	1	US-07-908-253-3
9	36.5	46.8	1403	2	US-08-694-865-17
10	36.5	46.8	1403	2	US-08-535-837-3
11	36.5	46.8	1403	3	US-09-124-491-17
12	36	46.2	300	3	US-08-727-688-11
13	36	46.2	1713	3	US-08-600-982-24
14	36	46.2	1713	4	PCT-US94-10261A-24
15	35	44.9	43	2	US-08-609-046A-2
16	35	44.9	43	2	US-08-609-046A-4
17	35	44.9	43	3	US-09-158-477-2
18	35	44.9	43	3	US-09-158-477-4
19	35	44.9	137	2	US-08-640-978C-1
20	35	44.9	137	2	US-08-640-978C-5
21	35	44.9	228	2	US-08-609-046A-1
22	35	44.9	228	3	US-08-609-046A-7
23	35	44.9	228	3	US-09-158-477-1
24	35	44.9	228	3	US-09-158-477-1
25	35	44.9	517	2	US-08-967-508-19
26	35	44.9	517	2	US-08-967-506-19
27	35	44.9	517	4	PCT-US94-02552-19
28	35	44.9	559	2	US-08-967-508-9

29	35	44.9	559	3	US-08-967-506-9	Sequence 9, Appl
30	35	44.9	559	3	PCT-US94-02552-9	Sequence 9, Appl
31	34	43.6	42	3	US-08-924-330A-2	Sequence 2, Appl
32	34	43.6	146	1	US-07-989-363-2	Sequence 2, Appl
33	34	43.6	146	1	US-08-264-526-2	Sequence 2, Appl
34	34	43.6	422	1	US-08-152-483B-3	Sequence 3, Appl
35	34	43.6	426	1	US-08-152-483B-7	Sequence 7, Appl
36	34	43.6	478	1	US-08-152-483B-9	Sequence 9, Appl
37	34	43.6	516	2	US-08-762-106-8	Sequence 8, Appl
38	34	43.6	516	3	US-08-745-404-2	Sequence 2, Appl
39	34	43.6	527	2	US-08-762-106-9	Sequence 9, Appl
40	34	43.6	552	3	US-08-745-404-3	Sequence 3, Appl
41	34	43.6	635	1	US-07-832-855-2	Sequence 2, Appl
42	34	43.6	707	3	US-08-704-711A-19	Sequence 19, Appl
43	34	43.6	970	2	US-08-673-789-7	Sequence 7, Appl
44	34	43.6	973	1	US-08-162-809-10	Sequence 10, Appl
45	34	43.6	988	1	US-08-162-809-14	Sequence 14, Appl

ALIGNMENTS

```
RESULT 1
US-08-464-340A-13
: Sequence 13, Application US/08464340A
: Patent No. 5710019
: GENERAL INFORMATION:
: APPLICANT: LI, ET AL.
: TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
: CECCHI, STEWART & OLSTEIN
: STREET: 6 BECKER FARM ROAD
: CITY: ROSELAND
: STATE: NEW JERSEY
: COUNTRY: USA
: ZIP: 07068
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 INCH DISKETTE
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WORD PERFECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/464,340A
: FILING DATE: June 5,1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/08449
: FILING DATE: 28 JUL 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: FERRARO, GREGORY D.
: REGISTRATION NUMBER: 36,134
: REFERENCE/DOCKET NUMBER: 325800-415
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-994-1700
: TELEFAX: 201-994-1744
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 539 AMINO ACIDS
: TYPE: AMINO ACID
: STRANDEDNESS:
: TOPOLOGY: LINEAR
: MOLECULE TYPE: PROTEIN
: US-08-464-340A-13

Query Match      65.4%; Score 51; DB 1; Length 539;
Best Local Similarity 66.7%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 1 FAEDERDSQFSPSP 15
||| ||| ||| |||
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Db 349 FAEKEDDTKFSIP 363

RESULT 2

US-08-527-152-2

Sequence 2, Application US/08527152

Patent No. 5627065

GENERAL INFORMATION:

APPLICANT: Chandu, Kanianthara G.

APPLICANT: Cahalan, Michael D.

APPLICANT: Glissmer, Stephan

APPLICANT: Goldin, Alan L.

APPLICANT: Delnells, Brent A.

APPLICANT: Gutman, George A.

APPLICANT: Wasmuth, John J.

TITLE OF INVENTION: Assay, Methods and Products Based On n

TITLE OF INVENTION: K+ Channel Expression

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,

ADDRESSEE: Attn: W.H. Dreger

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/527,152

FILING DATE: UNKNOWN

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/170,418

FILING DATE: 20-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/558,568

FILING DATE: 27-JUL-1990

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-54444-2/WHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 528 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-527-152-2

Query Match 59.0%; Score 46; DB 2; Length 528;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Db 371 FAEADPSSGFSIP 385

RESULT 3

US-08-288-405A-10

Sequence 10, Application US/08288405A

Patent No. 5559009

GENERAL INFORMATION:

APPLICANT: Chandu, Kanianthara G.

APPLICANT: Kalman, Katalin
APPLICANT: Chandu, Girscha
APPLICANT: Gutman, George A.
TITLE OF INVENTION: A No. 5559009el Voltage-gated Potassium Channel
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,

ADDRESSEE: Attn: Walter H. Dreger

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/288,405A

FILING DATE: 10-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/207,431

FILING DATE: 04-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-59844-1/WHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 532 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-288-405A-10

Query Match 57.7%; Score 45; DB 1; Length 532;
Best Local Similarity 60.0%; Pred. No. 2.4;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Db 408 FAEVDVDTHTFSIP 422

RESULT 4

US-07-789-915A-2

Sequence 2, Application US/07789915A

Patent No. 5212058

GENERAL INFORMATION:

APPLICANT: Baker, Rohan T.

APPLICANT: Varshavsky, Alexander

TITLE OF INVENTION: Ubiquitin-Specific Proteases

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millitia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS


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; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,915A
; FILING DATE: 19911108
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-5091AA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1121 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-789-915A-2

Query Match
Best Local Similarity 46.8%; Score 36.5; DB 1; Length 1121;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 FAEADERDSQFSPSIP 15
Db 601 YARVDE-DQPPFAPV 614

RESULT 5
US-08-005-002C-2
; Sequence 2, Application US/08005002C
; Patent No. 5494818
; GENERAL INFORMATION:
; APPLICANT: Baker, Rohan T.
; APPLICANT: Tobias, John W.
; APPLICANT: Varshavsky, Alexander
; TITLE OF INVENTION: Ubiquitin-Specific Proteases
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: U.S.A.
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/005,002C
; FILING DATE: 15-JAN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,915
; FILING DATE: 08-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: MIT-5091AA2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 207-363-0528
; TELEFAX: 207-363-0528
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1121 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-005-002C-2
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Query Match
Best Local Similarity 46.8%; Score 36.5; DB 1; Length 1121;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 FAEADERDSQFSPSIP 15
Db 601 YARVDE-DQPPFAPV 614

RESULT 6
US-08-487-203A-2
; Sequence 2, Application US/08487203A
; Patent No. 5683904
; GENERAL INFORMATION:
; APPLICANT: Baker, Rohan T.
; APPLICANT: Tobias, John W.
; APPLICANT: Varshavsky, Alexander
; TITLE OF INVENTION: Ubiquitin-Specific Proteases
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: U.S.A.
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,203A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/005,002
; FILING DATE: 15-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: MIT-5091AA32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 207-363-0528
; TELEFAX: 207-363-0528
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1121 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-203A-2

Query Match
Best Local Similarity 46.8%; Score 36.5; DB 1; Length 1121;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 FAEADERDSQFSPSIP 15
Db 601 YARVDE-DQPPFAPV 614

RESULT 7
5476657-1
; Patent No. 5476657
; APPLICANT: POTTER, ANDREW A.
; TITLE OF INVENTION: PASTURELLA HAEMOLYTICA LEUKOTOXIN
; COMPOSITIONS AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
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: APPLICATION NUMBER: US/08/15,537
: FILING DATE: 09-FEB-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 504,850
: FILING DATE: 05-APR-1990
: APPLICATION NUMBER: 335,018
: FILING DATE: 07-APR-1989
: SEQ ID NO:1:
: LENGTH: 1334
5476657-1

Query Match      46.8%; Score 36.5; DB 5; Length 1334;
Best Local Similarity 46.7%; Pred. No. 2.2e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

OY      1 FAEDERDSQFSP15
DB      883 YARVDE-DQPPAVP 896

RESULT      8
US-07-908-253-3
: Sequence 3, Application US/07908253
: Patent No. 5534256
: GENERAL INFORMATION:
: APPLICANT: POTTER, ANDREW A.
: APPLICANT: HARLAND, RICHARD J.
: TITLE OF INVENTION: HAEMOPHILUS SOMMUS OUTER MEMBRANE
: TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ROBERTA L. ROBINS
: STREET: 635 BRYANT STREET
: CITY: PALO ALTO
: STATE: CALIFORNIA
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/908,253
: FILING DATE: 19920702
: CLASSIFICATION: 420
: ATTORNEY/AGENT INFORMATION:
: NAME: ROBINS, ROBERTA L.
: REGISTRATION NUMBER: 33,208
: REFERENCE/DOCKET NUMBER: 9000-0026
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 617-8999
: TELEFAX: (415) 327-3231
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1403 amino acids
: TYPE: AMINO ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-908-253-3

Query Match      46.8%; Score 36.5; DB 1; Length 1403;
Best Local Similarity 46.7%; Pred. No. 2.4e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

OY      1 FAEDERDSQFSP15
DB      883 YARVDE-DQPPAVP 896
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RESULT      9
US-08-694-865-17
: Sequence 17, Application US/08694865
: Patent No. 5837268
: GENERAL INFORMATION:
: APPLICANT: POTTER, ANDREW A.
: APPLICANT: MANN, JOHN G.
: TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: REED & ROBINS LLP
: STREET: 285 HAMILTON AVENUE, SUITE 200
: CITY: PALO ALTO
: STATE: CA
: COUNTRY: USA
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/694,865
: FILING DATE: 09-AUG-1996
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: MCCracken, THOMAS P.
: REGISTRATION NUMBER: 38,548
: REFERENCE/DOCKET NUMBER: 9001-0016.22
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)327-3400
: TELEFAX: (415)327-3231
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1403 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-694-865-17

Query Match      46.8%; Score 36.5; DB 2; Length 1403;
Best Local Similarity 46.7%; Pred. No. 2.4e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

OY      1 FAEDERDSQFSP15
DB      883 YARVD-RDQPPAVP 896

RESULT      10
US-08-535-837-3
: Sequence 3, Application US/08535837
: Patent No. 5985289
: GENERAL INFORMATION:
: APPLICANT: POTTER, ANDREW A.
: APPLICANT: HARLAND, RICHARD J.
: TITLE OF INVENTION: HAEMOPHILUS SOMMUS OUTER MEMBRANE
: TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ROBERTA L. ROBINS
: STREET: 285 HAMILTON AVENUE, SUITE 200
: CITY: PALO ALTO
: STATE: CALIFORNIA
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
```

TELEPHONE: (415) 327-3400

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QY	7	RDSQFPST	14
	111	1111	
Db	128	RDSDFPST	135

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RESULT 13
US-08-600-982-24
; Sequence 24, Application US/08600982
; Patent No. 6120991
; GENERAL INFORMATION:
; APPLICANT: Carter, William G.
; APPLICANT: Gil, Susanna A.
; APPLICANT: Ryan, Maureen C.
; TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for
; TITLE OF INVENTION: Integrins
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
; STREET: 1420 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-8100
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,982
; FILING DATE: 02-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K.
; REGISTRATION NUMBER: 26,997
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-8100
; TELEFAX: (206) 224-0779
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1713 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: E170 protein as translated from sequence
; DESCRIPTION: of FIGURES 15A-15F, and as shown also in FIGURES
; DESCRIPTION: 19A-19R
US-08-600-982-24

Query Match          46.2%; Score 36; DB 3; Length 1713;
Best Local Similarity 77.8%; Pred. No. 3.7e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 AADERSQ 10
    |||:|:|
Db 372 AADKRESQ 380

RESULT 14
PCT-US94-10261A-24
; Sequence 24, Application PC/TUS9410261A
; GENERAL INFORMATION:
; APPLICANT: Carter, William G.
; APPLICANT: Gil, Susanna A.
; APPLICANT: Ryan, Maureen C.
; TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for
; TITLE OF INVENTION: Integrins
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
; STREET: 1420 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-8100
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10261A
FILING DATE: 02-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: E170 protein as translated from sequence of
DESCRIPTION: FIGURES 15A-15F, and as shown also in FIGURES 19A-19R
PCT-US94-10261A-24

Query Match          46.2%; Score 36; DB 4; Length 1713;
Best Local Similarity 77.8%; Pred. No. 3.7e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 AADERSQ 10
    |||:|:|
Db 372 AADKRESQ 380

RESULT 15
US-08-609-046A-2
; Sequence 2, Application US/08609046A
; Patent No. 5811298
; GENERAL INFORMATION:
; APPLICANT: RONALD DEPINHO AND NICHOLE SCHREIBER-AGUS
; TITLE OF INVENTION: REP-MAX PROTEIN HAVING ANTI-
; TITLE OF INVENTION: ONCOGENIC ACTIVITY AND USES THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
; STREET: 90 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE DISKETTE
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,046A
; FILING DATE: FEBRUARY 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ELIZABETH A. BOGOSIAN
; REGISTRATION NUMBER: 39,911
; REFERENCE/DOCKET NUMBER: 96700/398
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-5995
; TELEFAX: (212) 286-0854 or 286-0082
; TELETYPE: TWX 710-581-4766
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; DESCRIPTION:
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;
;   HYPOTHETICAL: YES
;   ANTI-SENSE: NO
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   IDENTIFICATION METHOD:
;   OTHER INFORMATION:
US-08-609-046A-2

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Query Match      44.9%; Score 35; DB 2; Length 43;
Best Local Similarity 42.9%; Pred. No. 7.8;
Matches 9; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

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QY 1 FAADDERD-----SOFPSIP 15
    | | | | |
Db 19 FLRRRRECECHGYASSFPSP 39

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Search completed: February 2, 2001, 10:36:29
Job time: 42 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:35:47 ; Search time 45.64 Seconds
(without alignments)
11.238 Million cell updates/sec

Title: US-09-273-217-1

Perfect score: 78
Sequence: 1 FAEADERDSQFPSP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq.36.*
1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT.*
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4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT.*
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20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	15	20	V42762 Rat potassium chan
2	51	65.4	495	20	V32014 Human cation chan
3	51	65.4	858	20	V32015 Human cation chan
4	46	59.0	15	20	V42765 Rat potassium chan
5	45	57.7	532	16	R82937 Mouse Kv1.7 voltag
6	40	51.3	616	20	V32013 Drosophila melanog
7	40	51.3	1724	21	V54373 cDNA sequence enco
8	39	50.0	190	11	R03988 Mr 22k peripheral
9	39	50.0	576	20	V49541 Human PRO201 (Nsp1
10	39	50.0	576	20	V49545 Human Nsp1 mutant
11	39	50.0	576	20	V49546 Human Nsp1 mutant
12	39	50.0	576	20	V49547 Human Nsp1 mutant

13	39	50.0	576	20	Y06477 Human tumour-assoc
14	39	50.0	576	21	V51932 Human PRO201 prote
15	39	50.0	576	21	V51939 Human PRO201 prote
16	37	47.4	173	20	V36238 Human secreted pro
17	37	47.4	238	21	V99415 Human PRO1410 (UNQ
18	37	47.4	438	19	W71488 Helicobacter polyp
19	37	47.4	896	13	R21580 Plasma membrane pr
20	36.5	46.8	1015	20	W97241 Protein encoded by
21	36.5	46.8	1015	20	W97243 Protein encoded by
22	36.5	46.8	1022	6	P50097 Fusion protein of
23	36.5	46.8	1076	20	V31768 HCMV UL45-E. coli
24	36.5	46.8	1121	14	R36728 Ubiquitin fusion p
25	36.5	46.8	1199	15	R26188 HVTa antigen. Tur
26	36.5	46.8	1217	15	R49832 beat-galactosidase
27	36.5	46.8	1334	12	R14481 Lkta::lacZ fusion p
28	36.5	46.8	1334	15	R50290 Human RNA-associa
29	36.5	46.8	1403	12	R10890 Human membrane cha
30	36.5	46.8	1403	19	W79574 Leukotoxin 101. S
31	36	46.2	18	19	W54426 Human p5112 protei
32	36	46.2	101	20	Y29132 Amino acid sequenc
33	36	46.2	315	19	W71868 Amino acid encoded
34	36	46.2	315	19	W69384 Prostate tumour sp
35	36	46.2	315	21	Y82001 Human immunogenic
36	36	46.2	349	21	Y84617 Neisseria gonorrhoe
37	36	46.2	506	21	Y74417 Neisseria meningit
38	36	46.2	506	21	Y74418 Neisseria meningit
39	36	46.2	506	19	Y74419 Human PS112 protei
40	36	46.2	665	21	W54425 Human RNA-associa
41	36	46.2	670	21	Y70229 Human membrane cha
42	36	46.2	724	21	Y70451 Varicella zoster v
43	36	46.2	1310	15	R60292 VZV IEP 175. Vari
44	36	46.2	1310	15	R55798 P. falciparum PTEM
45	36	46.2	2228	20	W93944

ALIGNMENTS

RESULT 1	Y42762 standard; peptide; 15 AA.
ID	Y42762
XX	20-DEC-1999 (first entry)
AC	Rat potassium channel Kv1.2 vestibule-derived peptide #1.
DT	Ion channel; potassium channel; vestibule; inhibitor; antibody;
XX	polycyclonal; antagonist; hypertension; cardiac ischaemia;
DE	bronchial constriction; neurological diseases.
XX	Synthetic.
OS	Rattus sp.
XX	W09948927-A1.
PN	30-SEP-1999.
XX	19-MAR-1999; 99WO-US06019.
PF	25-MAR-1998; 98US-0079268.
PR	(CORR) CORNELL RES FOUND INC.
PA	Huang X;
XX	WPL: 1999-601205/51.
DR	Designing specific blockers that bind to the external vestibule region
XX	of ion channels, potentially useful for treating e.g. hypertension
PS	Claim 9; Page 8; 40pp; English.

XX This sequence represents a peptide (#1), derived from the extracellular
CC vestibule portion of the rat delayed rectifier potassium channel Kv1.2.
CC This was conjugated to keyhole limpet haemocyanin (KLH) and used to
CC generate polyclonal antibodies. The vestibule portion of potassium
CC channels is located on the extracellular portion of the channel protein,
CC and generally comprises a loop between the S5 transmembrane domain and
CC the pore forming region of the channel, or between the pore forming
CC region and the S6 transmembrane domain. The antibodies generated against
CC vestibule peptides act as potassium channel inhibitors by binding to the
CC vestibule portion, physically blocking the pore, or otherwise inducing a
CC conformational change in the channel. These potassium channel blockers
CC are potential therapeutic agents for e.g., hypertension, cardiac
CC ischaemia, bronchial constriction and neurological diseases. Such
CC inhibitors are specific for particular types of ion channel, and
CC are produced by rational design based on known nucleotide and amino acid
CC sequences for ion channels.
SQ Sequence 15 AA:

Query Match 100.0%; Score 78; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAEDERDSQFPSIP 15
DB 1 faeaderdsqfpsip 15
|||||

RESULT 2
Y32014
ID Y32014 standard; Protein; 495 AA.
XX Y32014;
AC Y32014;
XX 05-JAN-2000 (first entry)
DT
XX
DE Human cation channel protein.
XX
XX Cation channel protein; CCP; ion transport; arrhythmia;
KW diabetes mellitus; seizure; asthma; hypertension; therapy;
KW protein engineering; human.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Region 61..119
FT /note="crystal region"

XX WO9947923-A2.
XX
XX 23-SEP-1999.
XX
XX 22-MAR-1999; 99WO-US06307.
XX
XX 20-MAR-1998; 98US-0045529.
XX 02-APR-1998; 98US-0054347.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Mackinnon R;
XX
XX WPI: 1999-601131/51.
XX
XX Assays for screening compounds which interact with cation channel
PT proteins, useful for providing agents for treatment of diseases -
XX
XX Claim 21; Page 135-137; 165pp; English.
XX
XX The present sequence represents a human cation channel protein
CC (CCP). The invention provides an assay for screening potential
CC drugs or agents which interact with CCPs using prokaryotic CCPs

CC (such as those given in Y32009-12) mutated, using recombinant DNA
CC technology, to mimic the physiological function and chemical
CC properties of a functional eukaryotic CCP (such as those given in
CC Y32013-22). An example of a mutated prokaryotic CCP is given in
CC Y32024. The crystal region of the CCP may also be used in the
CC assay. The drugs or agents obtained can be used to treat
CC conditions related to the function of CCP in vivo, such as cardiac
CC arrhythmia, diabetes mellitus, seizure disorder, asthma or
CC hypertension. The invention has overcome the physical limitations
CC regarding the isolation and purification of eukaryotic CCPs.
XX
SQ Sequence 495 AA:

Query Match 65.4%; Score 51; DB 20; Length 495;
Best Local Similarity 66.7%; Pred. No. 0.57;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 FAEDERDSQFPSIP 15
DB 346 faeaderdsqfpsip 360
|||||

RESULT 3
Y32015
ID Y32015 standard; Protein; 858 AA.
XX Y32015;
AC Y32015;
XX 05-JAN-2000 (first entry)
DT
XX
DE Human cation channel protein.
XX
XX Cation channel protein; CCP; ion transport; arrhythmia;
KW diabetes mellitus; seizure; asthma; hypertension; therapy;
KW protein engineering; human.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Region 61..119
FT /note="crystal region"

XX WO9947923-A2.
XX
XX 23-SEP-1999.
XX
XX 22-MAR-1999; 99WO-US06307.
XX
XX 20-MAR-1998; 98US-0045529.
XX 02-APR-1998; 98US-0054347.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Mackinnon R;
XX
XX WPI: 1999-601131/51.
XX
XX Assays for screening compounds which interact with cation channel
PT proteins, useful for providing agents for treatment of diseases -
XX
XX Claim 21; Page 137-140; 165pp; English.
XX
XX The present sequence represents a human cation channel protein
CC (CCP). The invention provides an assay for screening potential
CC drugs or agents which interact with CCPs using prokaryotic CCPs.
CC (such as those given in Y32009-12) mutated, using recombinant DNA
CC technology, to mimic the physiological function and chemical
CC properties of a functional eukaryotic CCP (such as those given in
CC Y32013-22). An example of a mutated prokaryotic CCP is given in
CC Y32024. The crystal region of the CCP may also be used in the
CC assay. The drugs or agents obtained can be used to treat
CC conditions related to the function of CCP in vivo, such as cardiac

CC arrhythmia, diabetes mellitus, seizure disorder, asthma or
CC hypertension. The invention has overcome the physical limitations
CC regarding the isolation and purification of eukaryotic cDNA's.

XX Sequence 858 AA;

Query Match 65.4%; Score 51; DB 20; Length 858;

Best Local Similarity 66.7%; Pred. No. 1.1;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAEADERDSQSPSIP 15

DB 351 faeadedtkfsip 365

RESULT 4

Y42765

Y42765 standard; peptide: 15 AA.

AC Y42765;

DT 20-DEC-1999 (first entry)

DE Rat potassium channel Kv1.3 vestibule-derived peptide #4.

XX Ion channel; potassium channel; vestibule; inhibitor; antibody;

KW polyclonal; antagonist; hypertension; cardiac ischaemia;

KW bronchial constriction; neurological diseases.

XX Synthetic.

OS Rattus sp.

XX W09948927-A1.

XX 30-SEP-1999.

XX 19-MAR-1999; 99WO-US06019.

XX 25-MAR-1998; 98US-0079268.

PA (CORR) CORNELL RES FOUND INC.

XX Huang X;

XX WPI; 1999-601205/51.

DR Designing specific blockers that bind to the external vestibule region
XX of ion channels, potentially useful for treating e.g. hypertension -

PS Claim 9; Page 9; 40pp; English.

XX This sequence represents a peptide (#4), derived from the
CC extracellular vestibule portion of the rat potassium channel Kv1.3.
CC This was conjugated to keyhole limpet haemocyanin (KLH) and used to
CC generate polyclonal antibodies. The vestibule portion of potassium
CC channels is located on the extracellular portion of the channel protein,
CC and generally comprises a loop between the S5 transmembrane domain and
CC the pore forming region of the channel, or between the pore forming
CC region and the S6 transmembrane domain. The antibodies generated against
CC vestibule peptides act as potassium channel inhibitors by binding to the
CC vestibule portion, physically blocking the pore, or otherwise inducing a
CC conformational change in the channel. These potassium channel blockers
CC are potential therapeutic agents for e.g., hypertension, cardiac
CC ischaemia, bronchial constriction and neurological diseases. Such
CC inhibitors are specific for particular types of ion channel, and
CC are produced by rational design based on known nucleotide and amino acid
CC sequences for ion channels.

XX Sequence 15 AA;

Query Match 59.0%; Score 46; DB 20; Length 15;

Best Local Similarity 66.7%; Pred. No. 0.083;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 FAEADERDSQSPSIP 15

DB 1 faeaddptsgfsip 15

RESULT 5

R82937

R82937 standard; Protein: 532 AA.

AC R82937;

DT 10-APR-1996 (first entry)

DE Mouse Kv1.7 voltage-gated potassium channel.

XX Mouse Kv1.7 voltage-gated potassium channel;

KW insulin antagonist drug screening; insulin agonist drug screening;

KW non-insulin-dependent diabetes mellitus.

XX Mus musculus.

XX Key

FT Location/Qualifiers

FT 220..240

FT /note="putative membrane spanning domain (S1)"

FT 286..308

FT /note="putative membrane spanning domain (S2)"

FT 318..338

FT /note="putative membrane spanning domain (S3)"

FT 352..372

FT /note="putative membrane spanning domain (S4)"

FT 388..407

FT /note="putative membrane spanning domain (S5)"

FT 449..472

FT /note="putative membrane spanning domain (S6)"

FT 421..442

FT /note="pore-forming region"

FT 140..148

FT /note="tyrosine-kinase"

FT 380..382

FT /note="protein-kinase-C"

FT 384..386

FT /note="protein-kinase-C"

FT 267

FT /note="potential N-glycosylation site"

XX W09523858-A1.

XX 08-SEP-1995.

XX 23-FEB-1995; 95WO-US02221.

XX 10-AUG-1994; 94US-0288405.

XX 04-MAR-1994; 94US-0207401.

XX (REGC) UNIV CALIFORNIA.

XX Chandry G, Chandry KG, Gutman GA, Kalman K;

XX WPI; 1995-320573/41.

XX N-PSDB; T04953.

XX New voltage-gated potassium channel gene - used to identify

XX material(s) which can increase insulin release e.g. for treating

XX non-insulin dependent diabetes mellitus.

XX Disclosure; Fig 1B; 38pp; English.

XX Mouse Kv1.7 is a Shaker-related voltage-gated potassium channel

XX (see Fig 1B). It may be used in drug screening for

XX identification of therapeutics which modulate the channel and,

Query Match 51.3% Score 40: DB 21: Length 1724;
Best Local Similarity 63.6% Pred. No. 1.8e+02;
Matches 7: Conservative 1: Mismatches 3: Indels 0: Gaps 0:

Oy 5 DERDSQFSPSP 15
11:111111
Db 1182 denesfpdpdp 1192

RESULT 8

R03988 standard; Protein: 190 AA.

R03988:

30-AUG-1990 (first entry)

Mr 22K peripheral membrane protein of S.mansonl.

Schistosoma mansoni; surface membrane antigens; vaccine;

Immune response; parasite; lambda-gli expression library.

Synthetic.

Key Location/Qualifiers

Misc-difference 190 /note= "Glu encoded by CAA according tho the

specification"

WO9002563-A.

22-MAR-1990.

06-SEP-1989: 89WO-GB01049.

07-SEP-1988: 88GB-0021001.

15-DEC-1988: 88GB-0029429.

21-MAR-1989: 89GB-0006513.

(MEDI-) MEDICAL RES COUNCIL.

Simpson A/G, Smithers SR;

WPI: 1990-115819/15.

N-PSDB: Q03887.

Vaccine against Schistosoma mansoni

comprising antigens present in surface membrane of adult worm

Disclosure: Fig 7: 54pp: English.

The sequence is a surface antigen of adult S.mansonl having Mr 22K

and was isolated from a lambda expression library. A vaccine against

the parasite can be prepared from its fusion protein product pref.

in combination with an adjuvant such as saponin.

Sequence 190 AA:

Query Match 50.0% Score 39: DB 11: Length 190;
Best Local Similarity 60.0% Pred. No. 23;
Matches 6: Conservative 2: Mismatches 2: Indels 0: Gaps 0:

Oy 6 ERDSQFSPSP 15
111:11:1
Db 88 erdgkfpklp 97

RESULT 9

Y49541 standard; Protein: 576 AA.

XX Y49541:

AC 12-JAN-2000 (first entry)

DT Human PRO201 (Nsp1) protein.

Human: PRO201: PRO308: Nsp1: Nsp2: Nsp3: SH2 domain: EST:

expressed sequence tag; tumour; tumorigenesis; diagnosis; cancer;

identification; proliferation; neoplastic cell growth.

Homo sapiens.

WO954467-A1.

28-OCT-1999.

23-APR-1999: 99WO-US08847.

23-APR-1998: 98US-0082767.

22-DEC-1998: 98US-0113296.

(GETH) GENENTECH INC.

Stewart TA, Lu Y;

WPI: 1999-620728/53.

N-PSDB: Z32137.

New human polypeptides useful to screen for antagonists and produce

antibodies useful to diagnose and treat tumors, e.g. cancers

Claim 20: Fig 1; 152pp; English.

The present invention describes human proteins designated PRO201, PRO308

and PRO309, (also designated Nsp1, Nsp2 and Nsp3 respectively) which are

encoded by cDNA clones DNA30676, DNA40575 and DNA61601. The proteins

were shown to be encoded by genes that are amplified in the genome of

tumour cells, and are therefore believed to be useful targets for the

diagnosis and/or treatment (including prevention) of benign and malignant

tumours e.g. cancers in mammals, especially humans. They can be used to

produce anti-PRO201, anti-PRO308 or anti-PRO309 antibodies useful

(optionally combined with radiation treatment or a cytotoxic or

chemotherapeutic agent) to inhibit the growth of tumour cells or to treat

e.g. leukaemias, and immunologic disorders. The antibodies (especially in

growth inhibitory amounts) can also be included with a carrier and

optionally a second antibody or cytotoxic/chemotherapeutic agent in

compositions useful as above. They can be used to detect the proteins in

cells, by contacting the cell with the antibody and detecting binding,

useful to diagnose tumours in mammals (by contacting the antibody with a

tissue sample and detecting complex formation). Such diagnosis is

especially useful in mammals suspected of having neoplastic cell growth

or proliferation. The present sequence represents PRO201 (Nsp1).

Sequence 576 AA:

Query Match 50.0% Score 39: DB 20: Length 576;
Best Local Similarity 87.5% Pred. No. 78;
Matches 7: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

Oy 8 DSQFSPSP 15
11111111
Db 82 deqfspsp 89

RESULT 10

Y49545 standard; Protein: 576 AA.

Y49545:

12-JAN-2000 (first entry)

XX	Human Nsp1 mutant Nsp1-Y61F.
DE	
XX	
KM	Human; PRO201, PRO308; PRO309; Nsp1; Nsp2; Nsp3, SH2 domain; EST;
KM	expressed sequence tag; tumour; tumourigenesis; diagnosis; cancer;
KM	identification; proliferation; neoplastic cell growth; mutant.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PM	W09954467-A1.
PD	28-OCT-1999.
XX	
PF	23-APR-1999; 99WO-US08847.
XX	
PR	23-APR-1998; 98US-0082767.
PR	22-DEC-1998; 98US-0113296.
XX	
PA	(GENTH) GENENTECH INC.
XX	
PI	Stewart TA, Lu Y;
XX	
DR	WPI, 1999-620728/53.
XX	
PT	New human polypeptides useful to screen for antagonists and produce
PT	antibodies useful to diagnose and treat tumors, e.g. cancers -
XX	
PS	Example 4; Page 139-140; 152pp; English.
XX	
CC	The present invention describes human proteins designated PRO201, PRO308
CC	and PRO309, (also designated Nsp1, Nsp2 and Nsp3 respectively) which are
CC	encoded by cDNA clones DNA30676, DNA40575 and DNA61601. The proteins
CC	were shown to be encoded by genes that are amplified in the genome of
CC	tumour cells, and are therefore believed to be useful targets for the
CC	diagnosis and/or treatment (including prevention) of benign and malignant
CC	tumours e.g. cancers in mammals, especially humans. They can be used to
CC	produce anti-PRO201, anti-PRO308 or anti-PRO309 antibodies useful
CC	(optionally combined with radiation treatment or a cytotoxic or
CC	chemotherapeutic agent) to inhibit the growth of tumour cells or to treat
CC	e.g. leukemias, and immunologic disorders. The antibodies (especially in
CC	growth inhibitory amounts) can also be included with a carrier and
CC	optionally a second antibody or cytotoxic/chemotherapeutic agent in
CC	compositions useful as above. They can be used to detect the proteins in
CC	cells, by contacting the cell with the antibody and detecting binding,
CC	useful to diagnose tumours in mammals (by contacting the antibody with a
CC	tissue sample and detecting complex formation). Such diagnosis is
CC	especially useful in mammals suspected of having neoplastic cell growth
CC	or proliferation. The present sequence represents the human Nsp1 mutant
CC	Nsp1-Y61F, which is used in an example from the present invention.
XX	
SO	Sequence 576 AA:
XX	
Query Match	50.0%; Score 39; DB 20; Length 576;
Best Local Similarity	87.5%; Pred. No. 78;
Matches 7; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	8 DSQFPSIP 15
	I I I I I I I
Db	82 deqfslp 89
XX	
RESULT 11	
ID	Y49546 standard; Protein: 576 AA.
AC	Y49546;
XX	
DT	12-JAN-2000 (first entry)
XX	
DE	Human Nsp1 mutant Nsp1-Y95F.

KM	Human: PRO201, PRO308; PRO309; Nsp1; Nsp2; Nsp3; SH2 domain; EST;
KW	expressed sequence tag; tumour; tumorigenesis; diagnosis; cancer;
KM	Identification: proliferation; neoplastic cell growth; mutant.
XX	
OS	Homo sapiens.
XX	
OS	Synthetic.
XX	
PN	W09954467-A1.
XX	
PD	28-OCT-1999.
XX	
PF	23-APR-1999; 99MO-US08847.
XX	
PR	23-APR-1998; 98US-0082767.
XX	
PR	22-DEC-1998; 98US-0113296.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Stewart TA, Lu Y;
XX	
DR	WPI; 1999-620728/53.
XX	
PT	New human polypeptides useful to screen for antagonists and produce
PT	antibodies useful to diagnose and treat tumors, e.g. cancers -
XX	
PS	Example 4; Page 141-142; 152pp; English.
XX	
CC	The present invention describes human proteins designated PRO201, PRO308
CC	and PRO309, (also designated Nsp1, Nsp2 and Nsp3 respectively) which are
CC	encoded by cDNA clones DNA30676, DNA0575 and DNA61601. The proteins
CC	are shown to be encoded by genes that are amplified in the genome of
CC	tumour cells, and are therefore believed to be useful targets for the
CC	diagnosis and/or treatment (including prevention) of benign and malignant
CC	tumours, e.g. cancers in mammals, especially humans. They can be used to
CC	produce anti-PRO201, anti-PRO308 or anti-PRO309 antibodies useful
CC	(optionally combined with radiation treatment or a cytotoxic or
CC	chemotherapeutic agent) to inhibit the growth of tumour cells or to treat
CC	e.g. leukemias, and immunologic disorders. The antibodies (especially in
CC	growth inhibitory amounts) can also be included with a carrier and
CC	optionally a second antibody or cytotoxic/chemotherapeutic agent in
CC	compositions useful as above. They can be used to detect the proteins in
CC	cells, by contacting the cell with the antibody and detecting binding, or
CC	useful to diagnose tumours in mammals (by contacting the antibody with a
CC	tissue sample and detecting complex formation). Such diagnosis is
CC	especially useful in mammals suspected of having neoplastic cell growth
CC	or proliferation. The present sequence represents the human Nsp1 mutant
CC	Nsp1-Y95F, which is used in an example from the present invention.
XX	
SO	Sequence 576 AA;
XX	
Query Match	50.0%; Score 39; DB 20; Length 576;
Best Local Similarity	87.5%; Pred. No. 78;
Matches 7; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY 8 DSQFPSIP 15	
I I I I I I I	
Db 82 deqfspi 89	
RESULT 12	
Y49547	
ID Y49547 standard; Protein; 576 AA.	
XX Y49547;	
XX	
DT 12-JAN-2000 (first entry)	
XX	
DE Human Nsp1 mutant Nsp1-Y231F.	
XX	
KW Human: PRO201, PRO308; PRO309; Nsp1; Nsp2; Nsp3; SH2 domain; EST;	
KW	expressed sequence tag; tumour; tumorigenesis; diagnosis; cancer;
KW	Identification: proliferation; neoplastic cell growth; mutant.

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XX OS Homo sapiens.
OS Synthetic.
XX PN WO9954467-A1.
XX PD 28-OCT-1999.
XX PF 23-APR-1999; 99WO-US08847.
XX PR 23-APR-1998; 98US-0082767.
XX PR 22-DEC-1998; 98US-0113296.
XX PA (GETH ) GENENTECH INC.
XX PI Stewart TA, Lu Y;
XX DR WPI; 1999-620728/53.
XX PT New human polypeptides useful to screen for antagonists and produce
XX PS antibodies useful to diagnose and treat tumors, e.g. cancers
XX PS Example 4; Page 143-144; 152pp; English.
XX CC The present invention describes human proteins designated PRO201, PRO308
XX CC and PRO309, (also designated Nsp1, Nsp2 and Nsp3 respectively) which are
XX CC encoded by cDNA clones DNA30676, DNA40575 and DNA61601. The proteins
XX CC were shown to be encoded by genes that are amplified in the genome of
XX CC tumour cells, and are therefore believed to be useful targets for the
XX CC diagnosis and/or treatment (including prevention) of benign and malignant
XX CC tumours e.g. cancers in mammals, especially humans. They can be used to
XX CC produce anti-PRO201, anti-PRO308 or anti-PRO309 antibodies useful
XX CC (optionally combined with radiation treatment or a cytotoxic or
XX CC chemotherapeutic agent) to inhibit the growth of tumour cells or to treat
XX CC e.g. leukemias, and immunologic disorders. The antibodies (especially in
XX CC growth inhibitory amounts) can also be included with a carrier and
XX CC optionally a second antibody or cytotoxic/chemotherapeutic agent in
XX CC compositions useful as above. They can be used to detect the proteins in
XX CC cells, by contacting the cell with the antibody and detecting binding,
XX CC useful to diagnose tumours in mammals (by contacting the antibody with a
XX CC tissue sample and detecting complex formation). Such diagnosis is
XX CC especially useful in mammals suspected of having neoplastic cell growth
XX CC or proliferation. The present sequence represents the human Nsp1 mutant
XX CC Nsp1-Y231F, which is used in an example from the present invention.
XX SQ Sequence 576 AA;

Query Match 50.0%; Score 39; DB 20; Length 576;
Best Local Similarity 87.5%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 DSQFSPSIP 15
DB 82 deqfssip 89
I | | | | |
Y06477
ID Y06477 standard; Protein: 576 AA.
XX AC Y06477;
XX DT 27-SEP-1999 (first entry)
XX DE Human tumour-associated protein PRO201.
XX KM PRO201; UNQ175; cancer; tumour; diagnosis; therapy; human.
XX OS Homo sapiens.
XX PN WO9935170-A2.
XX
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PD 15-JUL-1999.
XX PF 05-JAN-1999; 99WO-US00106.
XX PR 20-NOV-1998; 98US-0109304.
XX PR 05-JAN-1998; 98US-0070440.
XX PR 29-APR-1998; 98US-0083500.
XX PR 22-MAY-1998; 98US-0086414.
XX PR 10-JUN-1998; 98US-0088742.
XX PR 10-NOV-1998; 98US-0107783.
XX PA (GETH ) GENENTECH INC.
XX PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
XX PI Roy MA, Wood WI;
XX DR WPI; 1999-430385/36.
XX DR N-PSDB; X87254.
XX PT Antibody against proteins expressed in neoplastic cells, useful for
XX PS tumor diagnosis and treatment
XX PS Example 1; Fig 2; 162pp; English.
XX CC This sequence represents human PRO201 (UNQ175), encoded by the
XX CC novel cDNA clone DNA30676 (see X87254). Amplification of DNA30676
XX CC occurs in various lung and colon tumours and cell lines, suggesting
XX CC a significant role in tumour formation and growth. Antagonists
XX CC (e.g. antibodies) directed against PRO201 are expected to have
XX CC utility in cancer therapy. The invention identifies 14 genes (see
XX CC X87254-67) that are amplified in the genome of tumour cells. Such
XX CC amplification is expected to be associated with overexpression of
XX CC the gene product and to contribute to tumorigenesis. The encoded
XX CC proteins (see Y06477-90) may be useful targets for the diagnosis
XX CC and/or treatment (including prevention) of certain cancers, and may
XX CC act as predictors of the prognosis of tumour treatment. Antibodies
XX CC that bind the proteins are claimed and used in claimed cancer
XX CC diagnostic kits.
XX SQ Sequence 576 AA;

Query Match 50.0%; Score 39; DB 20; Length 576;
Best Local Similarity 87.5%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 DSQFSPSIP 15
DB 82 deqfssip 89
I | | | | |
Y51932
ID Y51932 standard; Protein: 576 AA.
XX AC Y51932;
XX DT 23-JUN-2000 (first entry)
XX DE Human PRO201 protein.
XX KM PRO201; human; NSP; SH2-containing protein; cytosolic; modulator;
XX KW Src Homology-2 containing protein; Nsp1; PRO308; Nsp2; PRO309; Nsp3;
XX KW cellular response; tumorigenesis; integrin stimulation; signalling.
XX OS Homo sapiens.
XX PN US6051403-A.
XX PD 18-APR-2000.
XX PF 04-AUG-1999; 99US-0369028.
XX
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PR 23-APR-1998; 9805-0065275.
XX
PA (GETH ) GENENTECH INC.
XX
PI Lu Y, Stewart TA;
XX
DR WPI; 2000-328246/28.
DR N-PSDB; 289573.
XX
XX New isolated nucleic acid molecules encoding novel Src Homology-2
PT containing proteins capable of modulating the activity of cellular
PT response to external signaling -
XX
XX Claim 1; Column 39-44; 63pp; English.
XX
XX This invention describes the novel isolated Src Homology-2 (SH2)
CC containing proteins (Nsp) (I) PRO201 (Nsp1), PRO308 (Nsp2) or PRO309
CC (Nsp3), respectively which have cytosstatic activity. (I) plays an
CC important role in modulating the cellular response to external stimuli.
CC (I) binds and affects e.g. block or modulate, an activity such as
CC regulation of tumorigenesis, response to stimulation by integrin
CC receptors, epidermal growth factor, insulin growth factor and through
CC other tyrosine receptor ligands, of cellular response to external
CC signaling. (I) is useful for producing antibodies, agonists and
CC antagonists to modulate the activity of cellular response to external
CC signaling. The encoding Nsp nucleotides are useful as hybridization
CC probes in chromosome and gene mapping, in cDNA library and in the
CC generation of anti-sense RNA and DNA. They are also useful for
CC preparing the Nsp proteins, for producing transgenic animals and for
CC gene therapy. NI are also useful for treating and diagnosing cells
CC associated with cell proliferative disorders. This sequence represents
CC the PRO201 protein described in the method of the invention.
XX
SQ Sequence 576 AA;

Query Match 50.0%; Score 39; DB 21; Length 576;
Best Local Similarity 87.5%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 DSQFPSIP 15
| | | | | | |
Db 82 deqfipsip 89

RESULT 15
Y51939
ID Y51939 standard; Protein; 576 AA.
XX
AC Y51939;
XX
DT 23-JUN-2000 (first entry)
XX
DE Human PRO201 protein.
XX
KW PRO201; human; Nsp; SH2-containing protein; cytosstatic; modulator;
KW Src Homology-2 containing protein; Nsp1; PRO308; Nsp2; PRO309; Nsp3;
KW cellular response; tumorigenesis; integrin stimulation; signaling.
XX
OS Homo sapiens.
XX
XX US6051690-A.
XX
XX 18-APR-2000.
XX
XX 23-APR-1998; 9805-0065275.
XX
XX 23-APR-1998; 9805-0065275.
XX
XX (GETH ) GENENTECH INC.
XX
XX Stewart TA, Lu Y;
XX

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DR WPI; 2000-328250/28.
DR N-PSDB; 289585.
XX
XX New isolated Src Homology-2 containing polypeptides (Nsp) capable of
PT binding and modulating cellular response to external signaling -
XX
XX Claim 1; Column 44-48; 63pp; English.
XX
XX This invention describes the novel isolated Src Homology-2 (SH2)
CC containing proteins (Nsp) (I) PRO201 (Nsp1), PRO308 (Nsp2) or PRO309
CC (Nsp3), respectively which have cytosstatic activity. (I) plays an
CC important role in modulating the cellular response to external stimuli.
CC (I) binds and affects e.g. block or modulate, an activity such as
CC regulation of tumorigenesis, response to stimulation by integrin
CC receptors, epidermal growth factor, insulin growth factor and through
CC other tyrosine receptor ligands, of cellular response to external
CC signaling. (I) is useful for producing antibodies, agonists and
CC antagonists to modulate the activity of cellular response to external
CC signaling. This sequence represents the PRO201 protein described in the
CC method of the invention.
XX
SQ Sequence 576 AA;

Query Match 50.0%; Score 39; DB 21; Length 576;
Best Local Similarity 87.5%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 DSQFPSIP 15
| | | | | | |
Db 82 deqfipsip 89

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Search completed: February 2, 2001, 10:38:00
Job time: 133 sec

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OM protein - protein search, using sw model

Run on: February 2, 2001, 10:41:47 ; Search time 20.39 Seconds
(without alignments)
23.757 Million cell updates/sec

Title: US-09-273-217-2

Sequence: 1 DPLRNXYFDRNRPS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	85	100.0	495 1	CIK1_HUMAN
2	85	100.0	495 1	CIK1_MOUSE
3	85	100.0	495 1	CIK1_RAT
4	85	100.0	499 1	CIK2_HUMAN
5	85	100.0	499 1	CIK2_MOUSE
6	85	100.0	499 1	CIK2_XENLA
7	85	100.0	523 1	CIK3_HUMAN
8	85	100.0	525 1	CIK3_RAT
9	85	100.0	528 1	CIK3_MOUSE
10	85	100.0	529 1	CIK6_HUMAN
11	85	100.0	530 1	CIK6_RAT
12	85	100.0	598 1	CIK5_RAB1T
13	85	100.0	601 1	CIK5_MUSPF
14	85	100.0	602 1	CIK5_MOUSE
15	85	100.0	602 1	CIK5_RAT
16	85	100.0	613 1	CIK5_HUMAN
17	85	100.0	653 1	CIK4_HUMAN
18	85	100.0	654 1	CIK4_MOUSE
19	85	100.0	654 1	CIK4_MOUSE
20	85	100.0	655 1	CIK4_MOUSE
21	85	100.0	660 1	CIK4_BOVIN
22	85	100.0	660 1	CIK4_MOUSE
23	85	100.0	660 1	CIK4_MOUSE
24	85	100.0	660 1	CIK4_MOUSE
25	85	100.0	660 1	CIK4_MOUSE
26	85	100.0	660 1	CIK4_MOUSE
27	85	100.0	660 1	CIK4_MOUSE
28	85	100.0	660 1	CIK4_MOUSE
29	85	100.0	660 1	CIK4_MOUSE
30	85	100.0	660 1	CIK4_MOUSE
31	85	100.0	660 1	CIK4_MOUSE
32	85	100.0	660 1	CIK4_MOUSE
33	85	100.0	660 1	CIK4_MOUSE

ALIGNMENTS

RESULT	ID	STANDARD	PRT	495 AA.
1	CIK1_HUMAN			
AC	009470;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1 (HUK1) (HBK1).			
GN	KCNAL.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN:			
RA	Ramaswami M., Gautam M., Kamb A., Rudy B., Tanouye M.A., Mathew M.K.;			
RT	"Human potassium channel genes: molecular cloning and functional expression.";			
RL	Mol. Cell. Neurosci. 1:214-223(1990).			
RN	[2]			
RP	VARIANTS AEMK PHE-174; SER-239; ILE-249 AND ALA-408.			
RX	MEDLINE=95144169; PubMed=7842011;			
RA	Browne D.L., Gancher S.T., Nutt J.G., Brunt E.R.P., Smith E.A., Kramer P., Litt M.;			
RT	"Episodic ataxia/myokymia syndrome is associated with point mutations in the human potassium channel gene, KCNAL.";			
RL	Nat. Genet. 8:136-140(1994).			
RN	[3]			
RP	VARIANTS AEMK ARG-177; ALA-226 AND ILE-404.			
RX	MEDLINE=98260872; PubMed=9600245;			
RA	Scheffer H., Brunt E.R.P., Mol G.J.J., van der Vlies P., Stulp R.P., Verling E., Mantel G., Aveyanov Y.N., Holstra R.M.W., Buys C.H.C.M.;			
RT	"Three novel KCNAL mutations in episodic ataxia type I families.";			
RL	Hum. Genet. 102:464-466(1998).			
CC	-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.			
CC	-1- SUBUNIT: HETEROOTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.			
CC	-1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.			
CC	-1- DISEASE: DEFECTS IN KCNAL ARE THE CAUSE OF MYOKYMIA WITH PERIODIC ATAXIA (AEMK) (PAROXYSMAL OR EPISODIC ATAXIA (EA)). A DISEASE CHARACTERIZED BY CONTINUOUS MUSCLE MOVEMENT (MYOKYMIA) AND PERIODIC ATAXIA.			
CC	-1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.			

CC -----
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CC -----
DR EMBL: L02750: AAA36139.1; -.
DR HSSP: P03621: 2IFN.
DR MIM: 176260. -.
DR MIM: 160120. -.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR003091; -.
DR PFM: PF00520: Ion_trans; 1.
DR PRINTS: PR00169: KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KM Glycoprotein; Multigene family; Phosphorylation; Disease mutation.
FT TRANSMEM 168 186 SEGMENT S1 (BY SIMILARITY).
FT TRANSMEM 221 242 SEGMENT S2 (BY SIMILARITY).
FT TRANSMEM 254 274 SEGMENT S3 (BY SIMILARITY).
FT TRANSMEM 290 309 SEGMENT S4 (BY SIMILARITY).
FT TRANSMEM 326 345 SEGMENT S5 (BY SIMILARITY).
FT TRANSMEM 387 408 SEGMENT S6 (BY SIMILARITY).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. .) (POTENTIAL).
FT MOD_RES 322 322 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 322 322 (POTENTIAL).
FT MOD_RES 445 445 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 174 174 V -> F (IN AEK).
FT MOD_RES 177 177 /FTID-VAR.001508.
FT MOD_RES 226 226 I -> R (IN AEK).
FT MOD_RES 239 239 /FTID-VAR.001509.
FT MOD_RES 249 249 T -> A (IN AEK).
FT MOD_RES 249 249 R -> S (IN AEK).
FT MOD_RES 404 404 /FTID-VAR.001511.
FT MOD_RES 408 408 F -> I (IN AEK).
FT MOD_RES 408 408 V -> I (IN AEK).
FT MOD_RES 408 408 /FTID-VAR.001512.
FT MOD_RES 408 408 V -> A (IN AEK).
FT MOD_RES 408 408 /FTID-VAR.001513.
FT MOD_RES 408 408 V -> A (IN AEK).
FT MOD_RES 408 408 /FTID-VAR.001514.
SQ SEQUENCE 495 AA: 56541 MW: 0A1B1AB0536F5CBA CRC64;
Query Match 100.0%; Score 85; DB 1; Length 495;
Best Local Similarity 100.0%; Pred. No. 2,6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DPLRNEYFEDNRPS 15
DB 74 DPLRNEYFEDNRPS 88
RESULT 2
CIRL_MOUSE
ID CIRL_MOUSE STANDARD; PRT: 495 AA.
AC P16388;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (MK1) (MBK1).
GN KCNA1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90161996; PubMed-2305265;
RA Chandry K.G., Williams C.B., Spencer R.H., Aguilar B.A.,
RA Ghanshani S., Tempel B.L., Gutman G.A.;

RT "A family of three mouse potassium channel genes with intronless
RT coding regions.";
RL Science 247:973-975(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TTSUB-BRAIN;
RX MEDLINE-88189348; PubMed-2451788;
RA Tempel B.L., Jan Y.N., Jan L.Y.;
RT Cloning of a probable potassium channel gene from mouse brain.";
RL Nature 332:837-839(1988).
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -I- SUBUNIT: HETEROTRIMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M30439: AAA39711.1; -.
DR EMBL: Y00305: CAA68408.1; -.
DR PIR: S06378; S06378.
DR PIR: A40090; A40090.
DR HSSP: P03621: 2IFN.
DR MGD: MGI:96654; KCNA1.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR003091; -.
DR PFM: PF00520: Ion_trans; 1.
DR PRINTS: PR00169: KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KM Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 168 186 SEGMENT S1.
FT TRANSMEM 221 242 SEGMENT S2.
FT TRANSMEM 254 274 SEGMENT S3.
FT TRANSMEM 290 309 SEGMENT S4.
FT TRANSMEM 326 345 SEGMENT S5.
FT TRANSMEM 387 408 SEGMENT S6.
FT CARBOHYD 207 207 N-LINKED (GLCNAC. .) (POTENTIAL).
FT MOD_RES 322 322 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 446 446 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 446 446 (POTENTIAL).
SQ SEQUENCE 495 AA: 56409 MW: C9249F130E943D3D CRC64;
Query Match 100.0%; Score 85; DB 1; Length 495;
Best Local Similarity 100.0%; Pred. No. 2,6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DPLRNEYFEDNRPS 15
DB 74 DPLRNEYFEDNRPS 88
RESULT 3
CIRL_RAT

ID CIRK1_RAT STANDARD; PRT: 495 AA.
AC P10499;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (1A) (RBK1) (RCK1).
GN KCNA1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE-89052659; PubMed-3191911;
RA Baumann A., Grube A., Ackermann A., Pongs O.;
RT "Structure of the voltage-dependent potassium channel is highly
RT conserved from Drosophila to vertebrate central nervous systems.";
RL EMBO J. 7:2457-2463(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE-89203264; PubMed-2539643;
RA Christie M.J., Adelman J.P., Douglass J., North R.A.;
RT "Expression of a cloned rat brain potassium channel in Xenopus
RT oocytes.";
RL Science 244:221-224(1989).
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -I- SUBUNIT: HETEROETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X12589; CAA31102.1; -;
DR EMBL: M26161; AAA41982.1; -;
DR PIR: AA1353; A41353.
DR PIR: S01161; S01161.
DR HSP: P03621; 21FN.
DR INTERPRO: IPR000636; -;
DR INTERPRO: IPR003091; -;
DR PFAW: PF00520; Ion trans; 1.
DR PRINTS: PR00169; KCHANNEL.
KM Glycoprotein; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 168 186 SEGMENT S1.
FT TRANSMEM 221 242 SEGMENT S2.
FT TRANSMEM 254 274 SEGMENT S3.
FT TRANSMEM 290 309 SEGMENT S4.
FT TRANSMEM 326 345 SEGMENT S5.
FT TRANSMEM 367 408 SEGMENT S6.
FT CARBOHD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 322 322 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 322 322 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 445 445 PHOSPHORYLATION (BY CAPK)

FT SQ SEQUENCE 495 AA; 56379 MW; 29804463133F5D31 CRC64; (POTENTIAL).
Query Match 100.0%; Score 85; DB 1; Length 495;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DPLRNEYFEDRRNRP 15
DB 74 DPLRNEYFEDRRNRP 88
RESULT 4
CIRK2_HUMAN STANDARD; PRT: 499 AA.
AC P16389;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1998 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.2 (RBK2) (HBK5) (NGK1)
DE (MK2) (HUKIV).
GN KCNA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX Ramswami M., Gautam M., Kamb A., Rudy B., Tanouye M.A.,
RA Mathew M.K.;
RT "Human potassium channel genes: molecular cloning and functional
RT expression.";
RL Mol. Cell. Neurosci. 1:214-223(1990).
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -I- SUBUNIT: HETEROETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC -----
DR EMBL: L02752; AAA36141.1; -;
DR HSP: P03621; 21FN.
DR MIM: 176262; -;
DR INTERPRO: IPR000636; -;
DR INTERPRO: IPR003091; -;
DR PFAW: PF00520; Ion trans; 1.
DR PRINTS: PR00169; KCHANNEL.
KM Glycoprotein; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 164 182 SEGMENT S1.
FT TRANSMEM 222 243 SEGMENT S2.
FT TRANSMEM 255 275 SEGMENT S3.
FT TRANSMEM 293 311 SEGMENT S4.

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FT TRANSMEM 328 347 SEGMENT S5.
FT TRANSMEM 389 411 SEGMENT S6.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RRS 449 449 PHOSPHORYLATION (BY CAPK)
(POTENTIAL).
SQ SEQUENCE 499 AA; 56716 MW; 4B03F1B46A826C39 CRC64;

Query Match 100.0%; Score 85; DB 1; Length 499;
Best Local Similarity 100.0%; Pred..No. 2.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRNRPS 15
Db 70 DPLRNEYFFDRNRPS 84

RESULT 5
CIRK2_MOUSE STANDARD; PRT; 499 AA.
ID CIRK2_MOUSE 002010:
AC P15386: 002010:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.2 (RBK2) (RCK5) (NGK1)
DE (MK2) (HUKIV).
GN KCNA2.
OS Mus musculus (Mouse), and Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-RAT;
RX MEDLINE-89255260; PubMed-2722779;
RA McKinnon D.;
RT "Isolation of a cDNA clone coding for a putative second potassium
channel indicates the existence of a gene family."
RL J. Biol. Chem. 264:8230-8236(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-RAT; TISSUE-BRAIN;
RX MEDLINE-90059914; PubMed-2555158;
RA Stuehmer W., Ruppersberg J.P., Schroeter K.H., Sakmann B.,
Stoecker M., Giese K.P., Perschke A., Baumann A., Pongs O.;
RT "Molecular basis of functional diversity of voltage-gated potassium
channels in mammalian brain."
RL EMBO J. 8:3235-3244(1989).
RN [3]
RP REVISIONS.
RA Ludwig J.;
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-RAT;
RX MEDLINE-91352097; PubMed-1715584;
RA Paulmichl M., Nasimith P., Herlitz R., Reed K., Boyle W.A.,
Nerbonne J.M., Peralta E.G., Clapham D.E.;
RT "Cloning and expression of a rat cardiac delayed rectifier potassium
channel."
RL Proc. Natl. Acad. Sci. U.S.A. 88:7892-7895(1991).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES-MOUSE;
RX MEDLINE-90161996; PubMed-2305265;
RA Chandry K.G., Williams C.B., Spencer R.H., Aguilar B.A.,
Ghanshani S., Tempel B.L., Gutman G.A.;
RT "A family of three mouse potassium channel genes with intronless
coding regions."
RL Science 247:973-975(1990).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE

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CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROPOLYMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
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CC -----
DR EMBL; J04731; AAA40819.1; -
DR EMBL; X16003; CAA34134.1; -
DR EMBL; M74449; AAA19867.1; -
DR EMBL; M30440; AAA39713.1; -
DR PIR; A33814; A33814.
DR PIR; S06709; S06709.
DR PIR; B40090; B40090.
DR HSSP; P03621; 21FN.
DR MGD; MGI:96659; KCNA2.
DR INTERPRO; IPR000636; -
DR INTERPRO; IPR003091; -
DR PRAM; PR00520; ion.trans. 1.
DR PRINTS; PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 164 182 SEGMENT S1.
FT TRANSMEM 222 243 SEGMENT S2.
FT TRANSMEM 255 275 SEGMENT S3.
FT TRANSMEM 293 311 SEGMENT S4.
FT TRANSMEM 328 347 SEGMENT S5.
FT TRANSMEM 389 411 SEGMENT S6.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RRS 449 449 PHOSPHORYLATION (BY CAPK)
(POTENTIAL).
FT CONFLICT 411 411 S -> F (IN REF. 4).
FT SEQUENCE 499 AA; 56700 MW; A8FEA6F3F59AFA2A CRC64;

Query Match 100.0%; Score 85; DB 1; Length 499;
Best Local Similarity 100.0%; Pred..No. 2.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRNRPS 15
Db 70 DPLRNEYFFDRNRPS 84

RESULT 6
CIRK2_XENLA STANDARD; PRT; 499 AA.
ID CIRK2_XENLA
AC P22739;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.2 (XSHN2).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91026051; PubMed=2223094;
RA Ribera A.B.;
RT "A potassium channel gene is expressed at neural induction.";
RL Neuron 5:691-701(1990).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC -----
DR EMBL: M35664; AAA49933.1; -.
DR PIR: JH0313; JH0313.
DR HSSP: P03621; 21FN.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR003091; -.
DR PFAM: PF00520; Ion.trans. 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT FT TRANSMEM 164 182 SEGMENT S1.
FT FT TRANSMEM 222 243 SEGMENT S2.
FT FT TRANSMEM 255 275 SEGMENT S3.
FT FT TRANSMEM 293 311 SEGMENT S4.
FT FT TRANSMEM 328 347 SEGMENT S5.
FT FT TRANSMEM 389 411 SEGMENT S6.
FT FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT MOD_RES 449 449 PHOSPHORYLATION (BY CAPK)
FT FT (POTENTIAL).
SQ SEQUENCE 499 AA; 56701 MW; 11415768038DCBB CRC64;
Query Match 100.0%; Score 85; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DPLRNEYFDRNRPS 15
DB 70 DPLRNEYFDRNRPS 84
RESULT 7
CIR3_HUMAN STANDARD: PRT; 523 AA.
AC P22001;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKIII)
DE (HLK3).
DE KCNA3 OR HGK5.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC [1]
RN SEQUENCE FROM N.A.
RP TISSUE=SKELTAL MUSCLE;
RX MEDLINE=91095456; PubMed=198682;
RA Phillips L.H., Hice R.E., Schaefer K., Lamendola J., Bell G.I.,
RA Nelson D.J., Steiner D.F.;
RT "Sequence and functional expression in Xenopus oocytes of a human
RT insulinoma and islet potassium channel.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:53-57(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPHOCYTES;
RX MEDLINE=92189730; PubMed=1547020;
RA Cai Y.-C., Osborne P.B., North R.A., Doolley D.C., Douglass J.;
RT "Characterization and functional expression of genomic DNA encoding
RT the human lymphocyte type n potassium channel.";
RL DNA Cell Biol. 11:163-172(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92235098; PubMed=1373731;
RA Attali B., Romey G., Honore E., Schmid-Alliana A., Mattei M.-G.,
RA Lesage F., Ricard P., Barhanin J., Lazdunski M.;
RT "Cloning, functional expression, and regulation of two K+ channels in
RT human T lymphocytes.";
RL J. Biol. Chem. 267:8650-8657(1992).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE=95130104; PubMed=7829094;
RA Polander K., Douglass J., Swanson R.;
RT "Confirmation of the assignment of the gene encoding Kv1.3, a
RT voltage-gated potassium channel (KCNA3) to the proximal short arm of
RT human chromosome 1.";
RL Genomics 23:295-296(1994).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HEMIPENTAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
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CC -----
DR EMBL: M5515; AAA36425.1; -.
DR EMBL: M38217; AAB88073.1; -.
DR EMBL: M85217; AAA59457.1; -.
DR EMBL: L23499; AAC31761.1; -.
DR HSSP: P03621; 21FN.
DR MIM: 176263; -.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR003091; -.
DR PFAM: PF00520; Ion.trans. 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

```


CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-90161996; PubMed-2305265;
 RA Chandry K.G., Williams C.B., Spencer R.H., Aguilar B.A.,
 RA Ghanshani S., Tempel B.L., Gutan G.A.;
 RT "A family of three mouse potassium channel genes with intronless
 RT coding regions";
 RL Science 247:973-975(1990).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
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 CC -----
 DR EMBL; M30441; AAA39716.1; -.
 DR HSSP; P03621; 2IFN.
 DR MGD; MGI:96660; KCNA3.
 DR INTERPRO; IPR000636; -.
 DR INTERPRO; IPR003091; -.
 DR PFAM; PF00520; Ion_trans.1.
 DR PRINTS; PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 188 206 SEGMENT S1.
 FT TRANSMEM 248 269 SEGMENT S2.
 FT TRANSMEM 281 301 SEGMENT S3.
 FT TRANSMEM 316 334 SEGMENT S4.
 FT TRANSMEM 351 370 SEGMENT S5.
 FT TRANSMEM 412 434 SEGMENT S6.
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 473 473 PHOSPHORYLATION (BY CAPK)
 FT (POTENTIAL).
 SQ SEQUENCE 528 AA; 58526 MW; CDB65F1515F9A731 CRC64;

Query Match 100.0%; Score 85; DB 1; Length 528;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFDRNRPS 15
 |||
 DB 94 DPLRNEYFDRNRPS 108

RESULT 10
 C1K6_HUMAN
 ID C1K6_HUMAN STANDARD; PRT; 529 AA.
 AC P17658;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.6 (HBR2).
 GN KCNA6.
 OS Homo sapiens (Human).
 OC Karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE-BRAIN;
 RX MEDLINE-90269208; PubMed-2347305;
 RA Grube A., Schroeter K.H., Ruppersberg J.P., Stocker M., Drewes T.,
 RA Becht S., Pongs O.;
 RT "Cloning and expression of a human voltage-gated potassium channel. A
 RT novel member of the RCK potassium channel family";
 RL EMBO J. 9:1749-1756(1990).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- MISCELLANEOUS: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; X17622; CAA35623.1; -.
 DR PIR; S15057; S15057.
 DR MIM; 176257; -.
 DR INTERPRO; IPR000636; -.
 DR INTERPRO; IPR003091; -.
 DR PFAM; PF00520; Ion_trans.1.
 DR PRINTS; PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 175 193 SEGMENT S1.
 FT TRANSMEM 263 284 SEGMENT S2.
 FT TRANSMEM 296 316 SEGMENT S3.
 FT TRANSMEM 340 360 SEGMENT S4.
 FT TRANSMEM 376 396 SEGMENT S5.
 FT TRANSMEM 437 457 SEGMENT S6.
 FT MOD_RES 511 511 PHOSPHORYLATION (BY CAPK)
 FT (PROBABLE).
 SQ SEQUENCE 529 AA; 58728 MW; CFF0710A1E9CD69F CRC64;

Query Match 100.0%; Score 85; DB 1; Length 529;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFDRNRPS 15
 |||
 DB 78 DPLRNEYFDRNRPS 92

RESULT 11
 C1K6_RAT
 ID C1K6_RAT STANDARD; PRT; 530 AA.
 AC P17659;
 DT 01-AUG-1990 (Rel. 15, Created)

DT 01-ANUG-1990 (Rel. 15, last sequence update)
 DT 15-JUL-1998 (Rel. 36, last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL.6 (RCK2) (KV2).
 GN KCVN6.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN CORTEX;
 RX MEDLINE=90269208; PubMed=2347305;
 RA Grupe A., Schroeter K.H., Ruppertsberg J.P., Stocker M., Drewe T.,
 RA Beek S., Pongs O.
 RT "Cloning and expression of a human voltage-gated potassium channel. A
 RT novel member of the RCK potassium channel family.";
 RL EMBO J. 9:1749-1756(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=90297965; PubMed=2361015;
 RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B.,
 RA Polander K., Luneau C.J., Antanavage J., Oliva C., Buhrow S.A.,
 RA Bennett C., Stein R.B., Kaczmarek L.M.;
 RT "Cloning and expression of cDNA and genomic clones encoding three
 RT delayed rectifier potassium channels in rat brain.";
 RL Neuron 4:929-939(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=9110598; PubMed=1993474;
 RA Kirsch G.E., Drewe J.A., Verna S., Brown A.M., Joho R.H.;
 RT "Electrophysiological characterization of a new member of the RCK
 RT family of rat brain K⁺ channels.";
 RL FEBS Lett. 278:55-60(1991).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- MISCELLANEOUS: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X17621; CAA35622.1; -;
 DR EMBL: M21159; AAA41499.1; ALT_SEQ.
 DR PIR: JH0167; JH0167.
 DR PIR: S12786; S12786.
 DR INTERPRO: IPR000636; -;
 DR PIR: PFO0520; IPR003091; -;
 DR PIR: PFO0520; IPR003091; -;
 DR PRINTS: PRO0169; KCHANEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 175 193 SEGMENT S1.
 FT TRANSMEM 264 285 SEGMENT S2.
 FT TRANSMEM 297 317 SEGMENT S3.
 FT TRANSMEM 341 361 SEGMENT S4.

FT TRANSMEM 377 397 SEGMENT S5.
 FT TRANSMEM 438 458 SEGMENT S6.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 222 222 PHOSPHORYLATION (BY CK2) (POTENTIAL).
 FT MOD_RES 512 512 PHOSPHORYLATION (BY CKP)
 FT MOD_RES 528 528 (PROBABLE).
 FT MOD_RES 528 528 PHOSPHORYLATION (BY CKP)
 FT CONFLICT 241 241 (POTENTIAL).
 FT CONFLICT 333 333 S -> L (IN REF. 3).
 FT CONFLICT 333 333 R -> G (IN REF. 2).
 SQ SEQUENCE 530 AA; 58883 MW; 30A9774B66C1DA5 CRC64;
 Query Match 100.0%; Score 85; DB 1; Length 530;
 Best Local Similarity 100.0%; Pred. No. 2,8e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DPLRNEYFFDRNRRPS 15
 DB 78 DPLRNEYFFDRNRRPS 92
 AC P50638;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL.5.
 GN KCVN5.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAPANESE WHITE; TISSUE-HEART;
 RX MEDLINE=96032538; PubMed=7556635;
 RA Sasaki Y., Ishii K., Nunoki K., Yamagishi T., Taira N.;
 RT "The voltage-dependent K⁺ channel (Kv1.5) cloned from rabbit heart
 RT and facilitation of inactivation of the delayed rectifier current by
 RT the rat beta subunit.";
 RL FEBS Lett. 372:20-24(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NEW ZEALAND WHITE; TISSUE-PORTAL VEIN;
 RA Clement-Chomienne O., Ishii K., Walsh M.P., Cole W.C.;
 RT "Rabbit portal vein Kv1.5.";
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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CC EMBL: D45025; BAA08082.1; -
CC EMBL: AF036943; AAC13312.1; -
CC HSSP: P03621; 2IFN.
DR INTERPRO: IPR000636; -
DR INTERPRO: IPR003091; -
DR PFAM: PF00520; Ion_trans. 1.
DR PRINTS: PR00169; KCHANNEL.
KW Glycophorin; Transmembrane; Ion transport; Voltage-gated channel;
KM Ionic channel; Multigene family; Phosphorylation.
FT TRANSMEM 235 253 SEGMENT S1.
FT TRANSMEM 310 330 SEGMENT S2.
FT TRANSMEM 341 362 SEGMENT S3.
FT TRANSMEM 383 404 SEGMENT S4.
FT TRANSMEM 419 440 SEGMENT S5.
FT TRANSMEM 480 501 SEGMENT S6.
FT DOMAIN 78 83 POLY-GLY.
FT DOMAIN 367 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 598 AA; 65475 MW; B06D235ACTA8E1F0 CRC64;

Query Match 100.0%; Score 85; DB 1; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPLRNEFFDRNRPS 15
Db 141 DPLRNEFFDRNRPS 155

RESULT 13
CIR5_MOUSE STANDARD; PRT: 601 AA.
AC P79197;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.5.
GN KCNA5.
OS Mus musculus furo (Ferret).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=HEART ATRIUM;
RA Schwiegel T., Polander K., Swanson R.;
RL Submitted (Jan-1996) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC EMBL: U45979; ABA4145.1; -
CC DR INTERPRO: IPR000636; -
CC DR INTERPRO: IPR003091; -
DR PFAM: PF00520; Ion_trans. 1.
DR PRINTS: PR00169; KCHANNEL.
KW Glycophorin; Transmembrane; Ion transport; Voltage-gated channel;
KM Ionic channel; Multigene family; Phosphorylation.
FT TRANSMEM 240 258 SEGMENT S1.
FT TRANSMEM 314 334 SEGMENT S2.
FT TRANSMEM 345 366 SEGMENT S3.
FT TRANSMEM 386 407 SEGMENT S4.
FT TRANSMEM 422 443 SEGMENT S5.
FT TRANSMEM 483 504 SEGMENT S6.
FT DOMAIN 370 375 POLY-GLY.
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 601 AA; 65889 MW; 14ZDB9F8CB843FE0 CRC64;

Query Match 100.0%; Score 85; DB 1; Length 601;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPLRNEFFDRNRPS 15
Db 146 DPLRNEFFDRNRPS 160

RESULT 14
CIR5_MOUSE STANDARD; PRT: 602 AA.
AC Q61762;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.5 (KVL1-5).
GN KCNA5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS; TISSUE=HEART;
RX MEDLINE=94043264; PubMed=8226976;
RA Attali B., Lesage F., Ziliani P., Guillemare E., Honore E.,
RA Waidmann R., Hugnot J.-P., Mattle M.-G., Lazdunski M., Barhanin J.;
RT "Multiple mRNA isoforms encoding the mouse cardiac Kvl-1.5 delayed
RT rectifier K+ channel.";
RL J. Biol. Chem. 268:24283-24289(1993).
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- ALTERNATIVE PRODUCTS: 3 ISOFORMS: KVL1-5 (SHOWN HERE), KVL1-5/3',
CC AND KVL1-5/3' ARE PRODUCED BY ALTERNATIVE SPLICING. KVL1-5/3' IS
CC NON-FUNCTIONAL BUT INHIBITS EXPRESSION OF KVL1-5.
CC -I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART AND MODERATELY
CC IN BRAIN. LOW LEVELS IN THYMUS, SKELETAL MUSCLE AND SPLEEN. NOT
CC EXPRESSED IN LIVER, LUNG OR KIDNEY.
CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 2, 2001, 10:39:07 ; Search time 62.83 Seconds
(without alignments)
27.982 Million cell updates/sec

Title: US-09-273-217-2

Sequence: 1 DPLRNEYFDRNRP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.rodent:*
- 12: sp.virus:*
- 13: sp.vertebrate:*
- 14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	476	6	Q08635 bos taurus
2	85	100.0	483	13	Q09PM8 Oryzomys latipes
3	85	100.0	483	13	Q09PM8 Oryzomys latipes
4	85	100.0	489	13	Q09PM8 Oryzomys latipes
5	85	100.0	499	6	Q09MYX3 Oryzomys latipes
6	85	100.0	515	5	Q16968 Oryzomys latipes
7	85	100.0	522	5	Q061335 Mus musculus
8	85	100.0	529	11	Q061923 Mus musculus
9	85	100.0	583	13	Q09XXO Oryzomys latipes
10	85	100.0	593	6	Q028248 Oryzomys latipes
11	85	100.0	597	6	Q09TS07 Oryzomys latipes
12	85	100.0	602	11	Q0921R6 Oryzomys latipes
13	85	100.0	662	13	Q09YX8 Oryzomys latipes
14	85	100.0	516	6	Q028656 Oryzomys latipes
15	80	94.1	359	5	Q024277 Oryzomys latipes
16	80	94.1	708	5	Q09VW29 Oryzomys latipes
17	77	90.6	512	5	Q026597 Oryzomys latipes
18	75	88.2	511	4	Q016322 Oryzomys latipes
19	75	88.2	725	6	Q028649 Oryzomys latipes

20	73	85.9	488	5	Q025376 Loligo opal
21	72	84.7	494	13	Q091830 Oryzomys latipes
22	68	80.0	499	6	Q028293 Canis familiaris
23	58	68.2	301	5	Q025071 Haemaphysalis
24	58	68.2	532	11	Q070259 Mus musculus
25	57	67.1	556	5	Q017535 Mus musculus
26	57	67.1	558	5	Q062350 Caenorhabditis
27	55	64.7	489	5	Q026041 Panulirus
28	54	63.5	206	5	Q076778 Haemaphysalis
29	54	63.5	452	5	Q076266 Hirudo medicinalis
30	54	63.5	484	5	Q022012 Caenorhabditis
31	54	63.5	514	5	Q076457 Aplysia californica
32	54	63.5	518	5	Q09YIC6 Oryzomys latipes
33	54	63.5	776	5	Q019464 Caenorhabditis
34	49	57.6	500	4	Q090H4 Homo sapiens
35	49	57.6	503	11	Q097557 Rattus norvegicus
36	49	57.6	504	11	Q060565 Mesocricetus
37	49	57.6	545	2	Q085159 Shigella flexneri
38	49	57.6	4226	5	Q0989H5 Plasmodium
39	46	54.1	323	5	Q00800 Caenorhabditis
40	45	52.9	487	5	Q026094 Poliovirus
41	45	52.9	670	5	Q077270 Drosophila
42	44	51.8	496	3	Q04919 Saccharomyces
43	44	51.8	1024	3	Q074889 Schistosoma
44	43.5	51.2	518	13	Q073606 Gallus gallus
45	43	50.6	63	6	Q09TV14 Oryzomys latipes

ALIGNMENTS

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RESULT 1
ID Q08635 PRELIMINARY: PRT: 476 AA.
AC Q08635;
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE POTASSIUM CHANNEL PROTEIN KVL2 (BKs) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92267180; PubMed=1587348;
RA Reid P.F., Pongs O., Dolly J.O.;
RT Cloning of a bovine voltage-gated K+ channel gene utilizing partial
RT amino acid sequence of a dendrotoxin-binding protein from brain
RT cortex.
RT FEBS Lett. 302:31-34(1992).
RL
RT
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
CC IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I- MISCELLANEOUS: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -I- SIMILARITY: BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC EMBL: X66185; CAA46953.1; -.
CC INTERPRO: IPR000636; -.
CC INTERPRO: IPR001622; -.
CC INTERPRO: IPR003091; -.
CC INTERPRO: IPR003131; -.
CC PFM: PFM00520; ion.trans; 1.
CC PFM: PFM0214; K.tetra; 1.
DR

```

DR PRINTS: PR00169; KCHANNEL.
KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycopoliprotein; Multigene family; Phosphorylation.
FT TRANSMEM 164 182 SEGMENT S1 (BY SIMILARITY).
FT TRANSMEM 222 243 SEGMENT S2 (BY SIMILARITY).
FT TRANSMEM 255 275 SEGMENT S3 (BY SIMILARITY).
FT TRANSMEM 293 311 SEGMENT S4 (BY SIMILARITY).
FT TRANSMEM 328 347 SEGMENT S5 (BY SIMILARITY).
FT TRANSMEM 389 411 SEGMENT S6 (BY SIMILARITY).
FT MOD_RES 449 449 PHOSPHORYLATION (BY CAPK).
FT CARBOHYD 38 38 (BY SIMILARITY).
FT CARBOHYD 207 207 POTENTIAL.
FT NON_TER 476 476 POTENTIAL.
SQ SEQUENCE 476 AA; 54152 MW; D350456A611C057D CRC64;

Query Match 100.0%; Score 85; DB 6; Length 476;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRNRPS 15
Db 70 DPLRNEYFFDRNRPS 84

RESULT 2
O9PWW8 PRELIMINARY; PRT; 483 AA.
AC O9PWW8:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE POTASSIUM CHANNEL SHAKER ALPHA SUBUNIT VARIANT CV1.4 (M).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INNER EAR;
RA Rajeevan M.S., Hu S., Sakai Y., Sokolowski B.H.A.;
RT "Cloning and expression of Shaker alpha and beta subunits during inner ear development."
RL Brain Res. Mol. Brain Res. 66:83-93(1999).
DR EMBL: AF084460; ADI17794.1; -.
DR HSSP: P15385; 12TO.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFAM: PF00520; Ion_trans; 1.
DR PFAM: PF02214; K_tetra; 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel.
SQ SEQUENCE 483 AA; 54289 MW; 394855F1A2F73366 CRC64;

Query Match 100.0%; Score 85; DB 13; Length 483;
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRNRPS 15
Db 229 DPLRNEYFFDRNRPS 243

RESULT 3
O91829 PRELIMINARY; PRT; 483 AA.
AC O91829:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE SHAKER-RELATED POTASSIUM CHANNEL TSHAZ.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=98146169; PubMed=9486764;
RA Nguyen T.D., Jeserich G.;
RT "Molecular structure and expression of shaker type potassium channels in glial cells of trout CNS."
RL J. Neurosci. Res. 51:284-292(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Nguyen T.D., Jeserich G.;
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF252302; AAF70088.1; -.
KW Ionic channel.
SQ SEQUENCE 483 AA; 54955 MW; 68A78AEC44424956 CRC64;

Query Match 100.0%; Score 85; DB 13; Length 483;
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRNRPS 15
Db 71 DPLRNEYFFDRNRPS 85

RESULT 4
O91781 PRELIMINARY; PRT; 489 AA.
AC O91781:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE POTASSIUM CHANNEL.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LARYNGEAL MUSCLE;
RX MEDLINE=94045927; PubMed=8229210;
RA Ribeiro A.B., Nguyen D.A.;
RT "Primary sensory neurons express a Shaker-like potassium channel gene."
RL J. Neurosci. 13:4988-4996(1993).
DR EMBL: M94258; AAA16340.1; -.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR001622; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFAM: PF00520; Ion_trans; 1.
DR PFAM: PF02214; K_tetra; 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel.
SQ SEQUENCE 489 AA; 55995 MW; 5C5DD41334D58A43 CRC64;

Query Match 100.0%; Score 85; DB 13; Length 489;
Best Local Similarity 100.0%; Pred. No. 9.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRNRPS 15

Db 71 DPLRNEYFDRNRPS 85

RESULT 5

ID Q9MYX3 PRELIMINARY; PRT; 499 AA.

AC Q9MYX3;

DT 01-OCT-2000 (TREMBLrel. 15, Created).

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DE POTASSIUM CHANNEL SUBUNIT KV 1.2.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RA Thorneloe K.S., Walsh M.P., Cole W.C.;

RT "Rabbit portal vein KV 1.2."

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF284420; AAF91476.1; --

SQ SEQUENCE 499 AA; 56692 MW; 7A4BF46D8FB36308 CRC64;

Query Match 100.0%; Score 85; DB 6; Length 499;
 Best Local Similarity 100.0%; Pred. No. 9.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFDRNRPS 15

Db 70 DPLRNEYFDRNRPS 84

ID Q16968 PRELIMINARY; PRT; 515 AA.

AC Q16968;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE POTASSIUM CHANNEL.

OS Aplysia californica (California sea hare).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;

OC Aplysiidae; Aplysia.

OX NCBI_TaxID=6500;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=91186212; PubMed=2010814;

RA Pfaffinger P.J., Furukawa Y., Zhao B., Dugan D., Kandel E.R.;

RT "Cloning and expression of an Aplysia K+ channel and comparison with

RT native Aplysia K+ currents."

RL J. Neurosci. 11:918-927(1991).

DR EMBL: M95914; AAA2756.1; --

DR INTERPRO: IPR000636; --

DR INTERPRO: IPR001622; --

DR INTERPRO: IPR003091; --

DR INTERPRO: IPR003131; --

DR PFWAM: PF00520; Ion_trans; 1.

DR PFWAM: PF02214; K_tetra; 1.

DR PRINTS: PR00169; KCHANNEL.

KW Ionic channel.

SQ SEQUENCE 515 AA; 58539 MW; 76F6579C4C4D91E4 CRC64;

Query Match 100.0%; Score 85; DB 5; Length 515;
 Best Local Similarity 100.0%; Pred. No. 1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFDRNRPS 15

Db 103 DPLRNEYFDRNRPS 117

RESULT 7
 ID 061335 PRELIMINARY; PRT; 522 AA.

AC 061335;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DE POTASSIUM CHANNEL.

OS SHAKER.

OS Panulirus interruptus (California spiny lobster).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;

OC Palinuroidea; Palinuridae; Panulirus.

OX NCBI_TaxID=6735;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97477441; PubMed=9334397;

RA Kim M., Baro D.J., Lanning C.C., Doshi M., Farnham J., Moskowitz H.S.,

RA Peck J.H., Olivera B.M., Harris-Warrick R.M.;

RT "Alternative splicing in the pore-forming region of shaker potassium

RT channels."

RL J. Neurosci. 17:8213-8224(1997).

RN [2]

RP SEQUENCE FROM N.A.

RA Kim M.T., Baro D.J., Lanning C.C., Doshi M., Moskowitz H., Farnham J.,

RA Harris-Warrick R.M.;

RL Recept. Channels 0:0-0(1998).

DR EMBL: AF017129; AAC05909.1; --

DR INTERPRO: IPR000636; --

DR INTERPRO: IPR001622; --

DR INTERPRO: IPR003091; --

DR INTERPRO: IPR003131; --

DR PFWAM: PF00520; Ion_trans; 1.

DR PFWAM: PF02214; K_tetra; 1.

DR PRINTS: PR00169; KCHANNEL.

KW Ionic channel.

SQ SEQUENCE 522 AA; 59513 MW; 0FF0E7B233A33FBD CRC64;

Query Match 100.0%; Score 85; DB 5; Length 522;
 Best Local Similarity 100.0%; Pred. No. 1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFDRNRPS 15

Db 91 DPLRNEYFDRNRPS 105

ID Q61923 PRELIMINARY; PRT; 529 AA.

AC Q61923;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE MORINE POTASSIUM CHANNEL PROTEIN.

OS MK1.6.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Migeon M.B., Street V.A., Demas V.P., Tempel B.L.;

RL Epilepsy Res. 0:0-0(0).

DR EMBL: M96688; AAA39772.1; --

DR INTERPRO: IPR000636; --

DR INTERPRO: IPR001622; --

DR INTERPRO: IPR003091; --

DR PFWAM: PF00520; Ion_trans; 1.

DR PFWAM: PF02214; K_tetra; 1.

DR PRINTS: PR00169; KCHANNEL.

KW Ionic channel.
SQ SEQUENCE 529 AA; 58673 MW; 336D78C069ABEADD CRC64;

Query Match
Best Local Similarity 100.0%; Score 85; DB 11; Length 529;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
DB 78 DPLRNEYFFDRNRPS 92

RESULT 9
Q9XXX0 ID Q9XXX0 PRELIMINARY; PRT; 583 AA.
AC Q9XXX0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE TUKVI.
GN TUKVI.
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Scolidobranchia; Pyuridae; Halocynthia.
OX NCBI_Taxid=7729; [1]
RP SEQUENCE FROM N.A.
RA Ono F., Katayama Y., Nakajo K., Okamura Y.;
RT "Distinct mechanism controlling Na and K channel expression in a
developing neuronal blastomere."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB020853; BAA78383.1; -
DR INTERPRO; IPR000636; -
DR INTERPRO; IPR001622; -
DR INTERPRO; IPR003091; -
DR PFAM; PF00520; Ion_trans; 1.
DR PRINTS; PR00169; KCHANNEL.
SQ SEQUENCE 583 AA; 65935 MW; D9D00B42373B7EFD CRC64;

Query Match
Best Local Similarity 100.0%; Score 85; DB 5; Length 583;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
DB 103 DPLRNEYFFDRNRPS 117

RESULT 10
Q28248 ID Q28248 PRELIMINARY; PRT; 593 AA.
AC Q28248;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE DELAYED RECTIFIER K+ CHANNEL (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615; [1]
RN SEQUENCE FROM N.A.
RC TISSUE-COLON.
RA Overurf K.E., Russell S.N., Carl A., Vogalis R., Hart P.J.,
RL Hume J.R., Sanders K.M., Horowitz B.;
Am. J. Physiol. 267:0-0(1994).
DR EMBL; U08596; AAA57320.1; -
DR HSSP; O54397; 1BL8.
DR INTERPRO; IPR000636; -
DR INTERPRO; IPR001622; -
DR INTERPRO; IPR003091; -

DR INTERPRO; IPR003131; -
DR PFAM; PF00520; Ion_trans; 1.
DR PFAM; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
KW Ionic channel.
FT NON_TER 593
SQ SEQUENCE 593 AA; 65617 MW; 056278731409B228 CRC64;

Query Match
Best Local Similarity 100.0%; Score 85; DB 6; Length 593;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
DB 143 DPLRNEYFFDRNRPS 157

RESULT 11
Q9TS07 ID Q9TS07 PRELIMINARY; PRT; 597 AA.
AC Q9TS07;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE BAK5-DELAYED RECTIFIER POTASSIUM CHANNEL KV1.5 HOMOLOG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBI_Taxid=9913; [1]
RN SEQUENCE FROM N.A.
RP MEDLINE-95046327; PubMed-7957920;
RA Garcia-Guzman M., Sala F., Criado M., Sala S.;
RT "A delayed rectifier potassium channel cloned from bovine adrenal
medulla. Functional analysis after expression in Xenopus oocytes and
in a neuroblastoma cell line."
RL FEBS Lett. 354:173-176(1994).
DR INTERPRO; IPR000636; -
DR INTERPRO; IPR001622; -
DR INTERPRO; IPR003091; -
DR INTERPRO; IPR003131; -
DR PFAM; PF00520; Ion_trans; 1.
DR PFAM; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
SQ SEQUENCE 597 AA; 65757 MW; DE55DF1B767C20A CRC64;

Query Match
Best Local Similarity 100.0%; Score 85; DB 6; Length 597;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
DB 142 DPLRNEYFFDRNRPS 156

RESULT 12
Q9ZIR6 ID Q9ZIR6 PRELIMINARY; PRT; 602 AA.
AC Q9ZIR6;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VENTRICULAR POTASSIUM CHANNEL KV1.5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090; [1]
RN SEQUENCE FROM N.A.
RP Tanaka H., Janzen K., Winkfein R.J., Fliset C., Clark B., Giles W.R.;


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RT "Cloning and functional expression of mouse heart K+ channel alpha-
RL subunits, Kv1.5, Kv4.2, and Kv4.3."
DR Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF108659; AAD13779.1; -.
DR HSSP; Q54397; 1BL8.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR001622; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFM; PF00520; Ion_trans; 1.
DR PFM; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR Ionic channel.
SO SEQUENCE 602 AA; 66579 MW; 02926E85DC022DDA CRC64;

Query Match
Best Local Similarity 100.0%; Score 85; DB 11; Length 602;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 148 DPLRNEYFFDRNRPS 162

RESULT 13
QYGX8 PRELIMINARY; PRT; 662 AA.
ID QYGX8;
AC QYGX8;
DT 01-MAY-1999 (TREMBlrel. 10; Created)
DT 01-MAY-1999 (TREMBlrel. 10; Last sequence update)
DE 01-OCT-2000 (TREMBlrel. 15; Last annotation update)
DE POTASSIUM CHANNEL SHAKER CKVI.4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-99197209; Pubmed-10095080;
RA Raleevan M.S., Hu S., Sakai Y., Sokolowski B.H.A.;
RT "Cloning and expression of Shaker alpha- and beta-subunits during
RT inner ear development."
RL Brain Res. Mol. Brain Res. 66:83-93(1999).
DR EMBL; U82365; AAD11454.1; -.
DR HSSP; P15385; 12TO.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR001622; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFM; PF00520; Ion_trans; 1.
DR PFM; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR Ionic channel.
SO SEQUENCE 662 AA; 74061 MW; 7DB994240DF58007 CRC64;

Query Match
Best Local Similarity 100.0%; Score 85; DB 13; Length 662;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 229 DPLRNEYFFDRNRPS 243

RESULT 14
Q28656 PRELIMINARY; PRT; 516 AA.
ID Q28656;
AC Q28656;
DT 01-NOV-1998 (TREMBlrel. 01; Created)
DT 01-NOV-1998 (TREMBlrel. 08; Last sequence update)

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DT 01-OCT-2000 (TREMBlrel. 15; Last annotation update)
DE GLIBENCLAMIDE-SENSITIVE VOLTAGE-GATED POTASSIUM CHANNEL.
GN Kv1.3-GLTB.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NEW ZEALAND WHITE;
RX MEDLINE-96249424; Pubmed-8647945;
RA Yao X., Chang A.Y., Boulpaep E.L., Segal A.S., Desir G.V.;
RT "Molecular cloning of a glibenclamide-sensitive, voltage-gated
RT potassium channel expressed in rabbit kidney."
RL J. Clin. Invest. 97:2525-2533(1996).
DR EMBL; U38240; AAC24718.1; -.
DR HSSP; Q54397; 1BL8.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR001622; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFM; PF00520; Ion_trans; 1.
DR PFM; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR Ionic channel.
SO SEQUENCE 516 AA; 57430 MW; 795E84998BCA7CAA CRC64;

Query Match
Best Local Similarity 96.5%; Score 82; DB 6; Length 516;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 82 DPLRNEYFFDRNRPS 96

RESULT 15
Q24277 PRELIMINARY; PRT; 359 AA.
ID Q24277;
AC Q24277;
DT 01-NOV-1996 (TREMBlrel. 01; Created)
DT 01-NOV-1996 (TREMBlrel. 01; Last sequence update)
DE 01-OCT-2000 (TREMBlrel. 15; Last annotation update)
DE POTASSIUM CHANNEL PROTEIN (FRAGMENT).
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-87273502; Pubmed-2440582;
RA Kamb A., Iverson L.E., Tanouye M.A.;
RT "Molecular characterization of Shaker, a Drosophila gene that encodes
RT a potassium channel."
RL Cell 50:405-413(1987).
DR EMBL; M17155; AAA70217.1; -.
DR FLYBASE; FBgn0003380; Sh.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFM; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR Ionic channel; Membrane.
FT NON_TER 1
FT NON_TER 359
SO SEQUENCE 359 AA; 42622 MW; C1380CECC4512A70 CRC64;

Query Match
Best Local Similarity 94.1%; Score 80; DB 5; Length 359;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Fri Feb 2 15:15:33 2001

us-09-273-217-2.rspt

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QY      1 DPLRNEYFFDRNRPS 15
          |||||
Db     166 DPLRNEYFFDRSRPS 180
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Search completed: February 2, 2001, 10:39:09
Job time: 198 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 2, 2001, 10:37:10 ; Search time 38.22 Seconds

(without alignments)
26.649 Million cell updates/sec

Title: US-09-273-217-2

Perfect score: 85

Sequence: 1 DPLRNEYFFDRNRPS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	476	2 S21144	potassium channel
2	85	100.0	489	2 I51532	potassium channel
3	85	100.0	495	2 I57680	potassium channel
4	85	100.0	495	2 A40090	potassium channel
5	85	100.0	495	2 B39113	potassium channel
6	85	100.0	499	2 JH0313	potassium channel
7	85	100.0	499	2 I77466	potassium channel
8	85	100.0	499	2 I84204	potassium channel
9	85	100.0	499	2 A33814	potassium channel
10	85	100.0	514	2 C49507	potassium channel
11	85	100.0	523	2 A38101	potassium channel
12	85	100.0	523	2 I52990	voltage-gated pota
13	85	100.0	525	2 A43531	potassium channel
14	85	100.0	528	2 I84205	potassium channel
15	85	100.0	529	2 S12787	potassium channel
16	85	100.0	530	2 JH0167	potassium channel
17	85	100.0	597	2 S51212	BAK5 protein - bov
18	85	100.0	598	2 S66669	potassium channel
19	85	100.0	602	2 A49507	potassium channel
20	85	100.0	602	2 JH0166	potassium voltage-
21	85	100.0	613	2 A56031	potassium channel
22	85	100.0	653	2 A39922	potassium channel
23	85	100.0	654	2 S11049	potassium channel
24	85	100.0	654	2 E39113	potassium channel
25	85	100.0	660	2 S24125	potassium channel
26	80	94.1	304	2 S02284	potassium channel
27	80	94.1	349	2 S00482	potassium channel
28	80	94.1	359	2 A27159	potassium channel
29	80	94.1	564	2 S01110	potassium channel

30	80	94.1	616	2 S00479	potassium channel
31	80	94.1	643	2 S00480	potassium channel
32	80	94.1	656	2 JH0193	potassium channel
33	68	80.0	499	2 A48672	delayed rectifier
34	57	67.1	558	2 T23991	hypothetical prote
35	55	64.7	489	2 J04787	shaw protein - Cal
36	55	64.7	498	2 A41359	potassium channel
37	55	64.7	498	2 S12748	potassium channel
38	54	63.5	484	2 T24238	hypothetical prote
39	54	63.5	776	2 T20896	hypothetical prote
40	46	54.1	323	2 T29032	hypothetical prote
41	45	52.9	670	2 T13739	probable hormone r
42	44	51.8	1024	2 T41415	probable leucine p
43	44	51.8	1323	2 A24534	regulatory protein
44	43	50.6	460	2 T27759	hypothetical prote
45	43	50.6	511	2 A46020	potassium channel

ALIGNMENTS

```
RESULT 1
S21144
potassium channel protein RCK5 - bovine (fragment)
N:Alternate names: potassium channel protein 2
C:Species: Bos primigenius taurus (cattle)
C>Date: 22-Nov-1993 #sequence_revision 05-Apr-1995 #text_change 05-Nov-1999
C:Accession: S21144; A23668; A33158
R:Reid, P.F.; Pongs, O.; Dolly, J.O.
FEBS Lett. 302, 31-34, 1992
A:Title: Cloning of a bovine voltage-gated K(+) channel gene utilising partial amino
A:Reference number: S21144; MUID:92267180
A:Accession: S21144
A:Molecule type: DNA
A:Residues: 1-476 <REI>
A:Cross-references: GB:X66185; NID:q395206; PIDN:CA446953.1; PID:q395207
A>Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 320-
R:Scott, V.E.S.; Pearce, D.N.; Keen, J.N.; Findlay, J.B.C.; Dolly, J.O.
J. Biol. Chem. 265, 20094-20097, 1990
A:Title: alpha-Dendrotoxin acceptor from bovine brain is a K(+) channel protein. Evid
A:Reference number: A23668; MUID:91056043
A:Accession: A23668
A:Molecule type: protein
A:Residues: 2-28 <SCO>
A:Newitt, R.A.; Houamed, K.M.; Rehm, H.; Tempel, B.L.
submitted to the Protein Sequence Database, February 1991
A:Reference number: A33158
A:Accession: A33158
A:Molecule type: protein
A:Residues: 2-27 <NEW>
C:Keywords: glycoprotein; transmembrane protein
F:38,207,466/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 100.0%; Score 85; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 70 DPLRNEYFFDRNRPS 84

RESULT 2
I5132
potassium channel - african clawed frog
C:Species: Xenopus laevis (african clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I5132
R:Ribera, A.B.; Nguyen, D.A.
J. Neurosci. 13, 4988-4996, 1993
A:Title: Primary sensory neurons express a Shaker-like potassium channel gene.
A:Reference number: I5132; MUID:94045927
```

A:Accession: I51532
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-489 <RIB>
A:Cross-references: GB:M94258; NID:g387892; PIDN:AAA16340.1; PID:g387893

Query Match 100.0%; Score 85; DB 2; Length 489;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DPLRNEYFFDRRPS 15
DB 71 DPLRNEYFFDRRPS 85

RESULT 3
157680
potassium channel KCNA1 - human
N:Alternate names: potassium channel protein HKC-1
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 08-Oct-1999
C:Accession: I57680; A60173
R:Ramashwami, M.; Gautam, M.; Kamp, A.A.; Rudy, B.; Tanouye, M.A.; Mathew, M.K.
Mol. Cell. Neurosci. 1, 214-223, 1990
A:Title: Human potassium channel genes: molecular cloning and functional expression.
A:Reference number: I57680
A:Accession: I57680
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-495 <RMB>
A:Cross-references: GB:L02750; NID:g186662; PIDN:AAA3139.1; PID:g186663
R:Freeman, S.N.; Conley, E.C.; Brennand, J.C.; Russell, N.J.W.; Brammar, W.J.
Biochem. Soc. Trans. 18, 891a, 1990
A:Title: Cloning and characterization of a cDNA encoding a human brain potassium channel.
A:Reference number: A60173; MUID:91192386
A:Accession: A60173
A:Molecule type: mRNA
A:Residues: 263-264, 266-314, 'R' <FRE>
C:Genetics:
A:Gene: GDB:KCNA1; RBK1; HUK1; MBK1; AEMK; KVL1.1
A:Cross-references: GDB:127903; OMIM:176260
A:Map position: 12p13-12p13

Query Match 100.0%; Score 85; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 6.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRRPS 15
DB 74 DPLRNEYFFDRRPS 88

RESULT 4
A40090
potassium channel KVL1.1 protein - mouse
N:Alternate names: potassium channel A; potassium channel MK1
C:Species: Mus musculus (house mouse)
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 05-Nov-1999
C:Accession: A40090; S06376; I60746
R:Chandy, K.G.; Williams, C.B.; Spencer, R.H.; Aguilar, B.A.; Ghanashan, S.; Tempel, B.L.
Science 247, 973-975, 1990
A:Title: A family of three mouse potassium channel genes with intronless coding regions.
A:Reference number: A40090; MUID:90161996
A:Accession: A40090
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-495 <CHA>
A:Cross-references: GB:M30439; NID:g199702; PIDN:AAA39711.1; PID:g199703
R:Tempel, B.L.; Jan, Y.N.; Jan, L.Y.
Nature 332, 837-839, 1988
A:Title: Cloning of a probable potassium channel gene from mouse brain.

A:Reference number: S06378; MUID:88189348
A:Accession: S06378
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-495 <TEM>
A:Cross-references: GB:Y00305; GB:M36456; NID:953605; PIDN:CAA6408.1; PID:g53606
A:Note: It is uncertain whether Met-1 or Met-4 is the initiator
C:Genetics:
A:Gene: MBK1; MK1
C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane
F:361-370/Domain: transmembrane beta strand #status predicted <TM1>
F:371-379/Domain: transmembrane beta strand #status predicted <TM2>
F:207/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 85; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 6.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRRPS 15
DB 74 DPLRNEYFFDRRPS 88

RESULT 5
B39113
potassium channel KVL1.1 - rat
N:Alternate names: potassium channel A; potassium channel RK1
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 05-Nov-1999
C:Accession: B39113; A41353; S01161
R:Roberts, S.L.; Tamkun, M.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
A:Title: Cloning and tissue-specific expression of five voltage-gated potassium channels.
A:Reference number: A39113; MUID:91156694
A:Accession: B39113
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:Molecule type: mRNA
A:Residues: 1-495 <ROB>
R:Christie, M.J.; Adelman, J.P.; Douglass, J.; North, R.A.
Science 244, 221-224, 1989
A:Title: Expression of a cloned rat brain potassium channel in Xenopus oocytes.
A:Reference number: A41353; MUID:89203264
A:Accession: A41353
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-495 <CHR>
A:Cross-references: GB:M26161; NID:g206490; PIDN:AAA41982.1; PID:g206491
R:Baumann, A.; Grube, A.; Ackermann, A.; Pongs, O.
EMBO J. 7, 2457-2463, 1988
A:Title: Structure of the voltage-dependent potassium channel is highly conserved from
A:Reference number: S01161; MUID:89052659
A:Accession: S01161
A:Molecule type: mRNA
A:Residues: 1-495 <BAU>
A:Cross-references: EMBL:X12589; NID:g55957; PIDN:CAA1102.1; PID:g55958
C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane
F:361-370/Domain: transmembrane beta strand #status predicted <TM1>
F:371-379/Domain: transmembrane beta strand #status predicted <TM2>
F:207/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 85; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 6.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRRPS 15
DB 74 DPLRNEYFFDRRPS 88

RESULT 6
JH0313

potassium channel protein XShaz - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C:Accession: JH0313
 R:Ribera, A.B.
 Neuron 5, 691-701, 1990
 A:Title: A potassium channel gene is expressed at neural induction.
 A:Reference number: JH0313; MUID:91026051
 A:Accession: JH0313
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-499 <Rib>

Query Match 100.0%; Score 85; DB 2; Length 499;
 Best Local Similarity 100.0%; Pred. No. 6.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
 |||
 Db 70 DPLRNEYFFDRNRPS 84

RESULT 7
 177466
 potassium channel - human
 C:Species: Homo sapiens (man)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C:Accession: 177466
 R:Ramseyhaml, M.; Gautam, M.; Kamb, A.A.; Rudy, B.; Tanouye, M.A.; Mathew, M.K.
 Mol. Cell. Neurosci. 1, 214-223, 1990
 A:Title: Human potassium channel genes: molecular cloning and functional expression.
 A:Reference number: 157680
 A:Accession: 177466
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-499 <RES>
 A:Cross-references: GB:L02752; NID:9186668; PIDN:AAA36141.1; PID:9186669

Query Match 100.0%; Score 85; DB 2; Length 499;
 Best Local Similarity 100.0%; Pred. No. 6.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
 |||
 Db 70 DPLRNEYFFDRNRPS 84

RESULT 8
 184204
 potassium channel protein MK2 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C:Accession: B40090; 184204
 R:Chandry, K.G.; Williams, C.B.; Spencer, R.H.; Aguilar, B.A.; Chanshani, S.; Tempel, B.L.
 Science 247, 973-975, 1990
 A:Title: A family of three mouse potassium channel genes with intronless coding regions.
 A:Reference number: A40090; MUID:90161996
 A:Accession: B40090
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-499 <CHA>
 A:Cross-references: GB:M30440; NID:9199706; PIDN:AAA39713.1; PID:9199707
 C:Genetics:
 A:Gene: MK2

Query Match 100.0%; Score 85; DB 2; Length 499;
 Best Local Similarity 100.0%; Pred. No. 6.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15

Db 70 DPLRNEYFFDRNRPS 84
 |||

RESULT 9
 A33814
 potassium channel Kv1.2 - rat
 M:Alternate names: potassium channel RCK5; potassium channel RK2; RAK
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 05-Nov-1999
 C:Accession: A33814; C39113; S06709; I59204
 R:McKinnon, D.
 J. Biol. Chem. 264, 8230-8236, 1989
 A:Title: Isolation of a cDNA clone coding for a putative second potassium channel ind
 A:Reference number: A33814; MUID:89255260
 A:Accession: A33814
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-499 <MCK>

A:Cross-references: GB:J04731; NID:9203154; PIDN:AAA40819.1; PID:9203155
 R:Roberts, S.L.; Tamkun, M.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
 A:Title: Cloning and tissue-specific expression of five voltage-gated potassium chan
 A:Reference number: A39113; MUID:91156694
 A:Accession: C39113
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
 A:Molecule type: mRNA
 A:Residues: 1-12,24-499 <ROB>
 R:Stuhmer, W.; Ruppersberg, J.P.; Schroeter, K.H.; Sakmann, B.; Stocker, M.; Gliese,
 EMBO J. 8, 3235-3244, 1989
 A:Title: Molecular basis of functional diversity of voltage-gated potassium channels
 A:Reference number: S06708; MUID:90059914
 A:Accession: S06709
 A:Molecule type: mRNA
 A:Residues: 1-247,'SC',250-261,'T',263-282,'HTNR',288-291,'T',293-499 <STU>
 A:Cross-references: EMBL:X16003
 R:Paulmichl, M.; Nasmith, P.; Hellmisse, R.; Reed, K.E.; Boyle, W.A.; Nerbonne, J.M.;
 Proc. Natl. Acad. Sci. U.S.A. 88, 7892-7895, 1991
 A:Title: Cloning and expression of a rat cardiac delayed rectifier potassium channel.
 A:Reference number: I59204; MUID:91352097
 A:Accession: I59204
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-410,'F',412-499 <RES>
 A:Cross-references: GB:M74449; NID:9206548; PIDN:AAA19867.1; PID:9206549
 A:Experimental source: heart atrium
 C:Genetics:
 A:Gene: RAK

C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane
 F:164-182/Domain: transmembrane #status predicted <TM1>
 F:222-243/Domain: transmembrane #status predicted <TM2>
 F:255-275/Domain: transmembrane #status predicted <TM3>
 F:288-311/Domain: transmembrane #status predicted <TM4>
 F:328-347/Domain: transmembrane #status predicted <TM5>
 F:363-372/Domain: transmembrane beta strand #status predicted <TM1>
 F:373-381/Domain: transmembrane beta strand #status predicted <TM2>
 F:389-411/Domain: transmembrane #status predicted <TM6>
 F:207/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:449/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre

Query Match 100.0%; Score 85; DB 2; Length 499;
 Best Local Similarity 100.0%; Pred. No. 6.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
 |||
 Db 70 DPLRNEYFFDRNRPS 84

RESULT 10
 C49507
 potassium channel Kv1.5, form 3 - mouse

C:Species: Mus musculus (house mouse)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: C49507
R:Altali, B.; Lesage, F.; Zilliani, P.; Guillemare, E.; Honore, E.; Walzmann, R.; Hugnot, J. Biol. Chem. 268, 24283-24289, 1993
A:Title: Multiple mRNA isoforms encoding the mouse cardiac Kv1-5 delayed rectifier K(+) A:Reference number: A49507; MUID:94043264
A:Accession: C49507
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-514 <ATT>
A:Cross-references: GB:L22218
C:Keywords: alternative splicing

Query Match 100.0%; Score 85; DB 2; Length 514;
Best Local Similarity 100.0%; Pred. No. 6.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFDRNRPS 15
Db 148 DPLRNEYFDRNRPS 162
|||||

RESULT 11
A38101
potassium channel KCNA3 - human
N:Alternate names: potassium channel HK3; potassium channel PCN3; shaker-related potass
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 05-Nov-1999
C:Accession: A38101; B38536
R:Altali, B.; Romey, G.; Honore, E.; Schmid-Alliana, A.; Matzel, M.G.; Lesage, F.; Ricard J. Biol. Chem. 267, 8650-8657, 1992
A:Title: Cloning, functional expression, and regulation of two K(+) channels in human T A:Reference number: A38101; MUID:92235098
A:Accession: A38101
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-523 <ATT>
A:Cross-references: GB:M85217; NID:q186664; PIDN:AAA59457.1; PID:q186665
R:Phillipson, L.H.; Hlce, R.E.; Schaefer, K.; Lamendola, J.; Bell, G.I.; Nelson, D.J.; St proc. Natl. Acad. Sci. U.S.A. 88, 53-57, 1991
A:Title: Sequence and functional expression in Xenopus oocytes of a human insulinoma and A:Reference number: A38536; MUID:91095456
A:Accession: B38536
A:Molecule type: DNA
A:Residues: 1-19, 'G', '21-36, 'V', '38-60, 'L', '62-90, 'V', '92-337, 'S', '339-418, 'S', '420-457, 'LS', '4 A:Cross-references: GB:M55515
C:Genetics:
A:Gene: GDB:KCNA3
A:Cross-references: GDB:128079; OMIM:176263
A:Map position: 1p21-1p13.3
C:Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; volt

Query Match 100.0%; Score 85; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFDRNRPS 15
Db 89 DPLRNEYFDRNRPS 103
|||||

RESULT 12
I52990
voltage-gated potassium channel - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I52990
R:Cal, Y.C.; Osborne, P.B.; North, R.A.; Dooley, D.C.; Douglass, J.
DNA Cell Biol. 11, 163-172, 1992
A:Title: Characterization and functional expression of genomic DNA encoding the human 1y

A:Reference number: I52990; MUID:92189730
A:Accession: I52990
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-523 <RRS>
A:Cross-references: GB:M38217; NID:q186670; PIDN:AAA88073.1; PID:q186671
C:Genetics:
A:Gene: HGKS

Query Match 100.0%; Score 85; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFDRNRPS 15
Db 89 DPLRNEYFDRNRPS 103
|||||

RESULT 13
A43531
potassium channel Kv1.3 - rat
N:Alternate names: potassium channel Kv3; potassium channel RCK3; potassium channel R C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 05-Nov-1999
C:Accession: A43531; JH0168; S06708
R:Douglass, J.; Osborne, P.B.; Cal, Y.C.; Wilkinson, M.; Christie, M.J.; Adelman, J.P J. Immunol. 144, 4841-4850, 1990
A:Title: Characterization and functional expression of a rat genomic DNA clone encodi A:Reference number: A43531; MUID:90278098
A:Accession: A43531
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-525 <DOU>
A:Cross-references: GB:M30312
R:Swanson, R.; Marshall, J.; Smith, J.S.; Williams, J.B.; Boyle, M.B.; Folander, K.; Neuron 4, 929-939, 1990
A:Title: Cloning and expression of cDNA and genomic clones encoding three delayed rec A:Reference number: JH0166; MUID:90297965
A:Accession: JH0168
A:Molecule type: DNA
A:Residues: 1-180, 'G', '182-525 <SMA>
A:Cross-references: GB:M31744; NID:g205104; PIDN:AAA41500.1; PID:g205105
A:Experimental source: brain
A>Note: only a list of differences from sequence S06708 is given
R:Stuenkel, W.; Ruppersberg, J.P.; Schroeter, K.H.; Sakmann, B.; Stocker, M.; Giese, EMBO J. 8, 3235-3244, 1989
A:Title: Molecular basis of functional diversity of voltage-gated potassium channels A:Reference number: S06708; MUID:90059914
A:Accession: S06708
A:Molecule type: mRNA
A:Residues: 1-105, 'L', '107-180, 'G', '182-525 <STU>
A:Cross-references: EMBL:X16001; NID:g57034; PIDN:CAA34132.1; PID:g57035
C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane F:185-203/Domain: transmembrane #status predicted <TM1>
F:245-266/Domain: transmembrane #status predicted <TM2>
F:278-298/Domain: transmembrane #status predicted <TM3>
F:313-331/Domain: transmembrane #status predicted <TM4>
F:348-367/Domain: transmembrane #status predicted <TM5>
F:383-392/Domain: transmembrane beta strand #status predicted <TM6>
F:393-401/Domain: transmembrane beta strand #status predicted <TM7>
F:409-431/Domain: transmembrane #status predicted <TM8>
F:470/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre

Query Match 100.0%; Score 85; DB 2; Length 525;
Best Local Similarity 100.0%; Pred. No. 7.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFDRNRPS 15
Db 91 DPLRNEYFDRNRPS 105
|||||

RESULT 14

184205

potassium channel protein MK3 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C:Accession: C40090; 184205

R:Chandy, K.G.; Williams, C.B.; Spencer, R.H.; Aguilar, B.A.; Chanshani, S.; Tempel, B.L

Science 247, 973-975, 1990

A>Title: A family of three mouse potassium channel genes with intronless coding regions.

A:Reference number: A40090; MUID:90161996

A:Accession: C40090

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-528 <CNA>

A:Cross-references: GB:M30441; NID:g199712; PIDN:AAA39716.1; PID:g199713

Query Match

100.0%; Score 85; DB 2; Length 528;

Best Local Similarity 100.0%; Pred. No. 7.1e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPLRNEYFFDRNRPS 15

|||||

Db 94 DPLRNEYFFDRNRPS 108

RESULT 15

S12787

potassium channel KCNA2 - human

N:Alternate names: potassium channel HBK2

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999

C:Accession: S12787; S15057

R:Grube, A.; Schroeter, K.H.; Ruppersberg, J.P.; Stocker, M.; Drewes, T.; Beckh, S.; Por

EMBO J. 9, 1749-1756, 1990

A>Title: Cloning and expression of a human voltage-gated potassium channel. A novel mem

A:Reference number: S12786; MUID:90269208

A:Accession: S12787

A:Molecule type: mRNA

A:Residues: 1-529 <GRU>

A:Cross-references: EMBL:X17622

R:Pongs, O.

submitted to the EMBL Data Library, November 1989

A:Reference number: S15057

A:Accession: S15057

A:Molecule type: mRNA

A:Residues: 1-57, 'T', '59-529 <PON>

A:Cross-references: EMBL:X17622; NID:g32032; PIDN:CAA35623.1; PID:g32033

C:Genetics:

A:Gene: GDB:KCNA2; HK4; KVL.2

A:Cross-references: GDB:128062; OMIM:176262

C:Keywords: glycoprotein; ion channel; transmembrane protein

F:175-193/Domain: transmembrane #status predicted <TM1>

F:263-284/Domain: transmembrane #status predicted <TM2>

F:296-316/Domain: transmembrane #status predicted <TM3>

F:340-358/Domain: transmembrane #status predicted <TM4>

F:376-395/Domain: transmembrane #status predicted <TM5>

F:437-458/Domain: transmembrane #status predicted <TM6>

Query Match

100.0%; Score 85; DB 2; Length 529;

Best Local Similarity 100.0%; Pred. No. 7.1e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPLRNEYFFDRNRPS 15

|||||

Db 78 DPLRNEYFFDRNRPS 92

Search completed: February 2, 2001, 10:37:11
Job time: 84 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 2, 2001, 10:36:29 ; Search time 34.98 Seconds

(without alignments)
7.700 Million cell updates/sec

Title: US-09-273-217-2

Sequence: 1 DPLRNEYFFDRNRPS 15

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Issued_Patents_AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	149	2	US-08-606-143-24
2	85	100.0	150	2	US-08-606-143-26
3	85	100.0	150	2	US-08-606-143-29
4	85	100.0	151	2	US-08-606-143-19
5	85	100.0	152	2	US-08-606-143-4
6	85	100.0	152	2	US-08-606-143-5
7	85	100.0	152	2	US-08-606-143-6
8	85	100.0	152	2	US-08-606-143-7
9	85	100.0	152	2	US-08-606-143-9
10	85	100.0	152	2	US-08-606-143-10
11	85	100.0	152	2	US-08-606-143-12
12	85	100.0	152	2	US-08-606-143-13
13	85	100.0	152	2	US-08-606-143-15
14	85	100.0	152	2	US-08-606-143-16
15	85	100.0	152	2	US-08-606-143-18
16	85	100.0	152	2	US-08-606-143-20
17	85	100.0	152	2	US-08-606-143-21
18	85	100.0	152	2	US-08-606-143-25
19	85	100.0	152	2	US-08-606-143-30
20	85	100.0	152	2	US-08-606-143-32
21	85	100.0	153	2	US-08-606-143-11
22	85	100.0	153	2	US-08-606-143-22
23	85	100.0	153	2	US-08-606-143-27
24	85	100.0	153	2	US-08-606-143-31
25	85	100.0	155	2	US-08-606-143-8
26	85	100.0	155	2	US-08-606-143-14
27	85	100.0	155	2	US-08-606-143-17
28	85	100.0	155	2	US-08-606-143-23

29	85	100.0	528	2	US-08-527-152-2	Sequence 2, Appl
30	82	96.5	152	2	US-08-606-143-28	Sequence 28, Appl
31	58	68.2	532	1	US-08-288-405A-10	Sequence 10, Appl
32	43	50.6	200	2	US-08-606-143-42	Sequence 42, Appl
33	43	50.6	513	1	US-08-464-340A-2	Sequence 2, Appl
34	43	50.6	513	4	PCT-US94-08449A-2	Sequence 2, Appl
35	42	49.4	179	2	US-08-606-143-33	Sequence 33, Appl
36	42	49.4	179	2	US-08-606-143-34	Sequence 34, Appl
37	42	49.4	179	2	US-08-606-143-35	Sequence 35, Appl
38	42	49.4	179	2	US-08-606-143-36	Sequence 36, Appl
39	42	49.4	539	1	US-08-464-340A-13	Sequence 13, Appl
40	41	48.2	190	2	US-08-606-143-37	Sequence 37, Appl
41	41	48.2	208	2	US-08-606-143-40	Sequence 40, Appl
42	40	47.1	494	1	US-08-464-340A-4	Sequence 4, Appl
43	40	47.1	494	4	PCT-US94-08449A-4	Sequence 4, Appl
44	37	43.5	162	2	US-08-606-143-44	Sequence 44, Appl
45	37	43.5	811	1	US-08-480-604A-7	Sequence 7, Appl

ALIGNMENTS

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RESULT 1
US-08-606-143-24
; Sequence 24, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: LI, Min
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELE: 25-3533
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-606-143-24

Query Match 100.0%; Score 85; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. NO. 1.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DPLRNEYFFDRNRPS 15
Db 39 DPLRNEYFFDRNRPS 53

```

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RESULT 2
US-08-606-143-26
: Sequence 26, Application US/08606143
: Patent No. 5856155
: GENERAL INFORMATION:
: APPLICANT: LI, MIN
: TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
: TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
: TITLE OF INVENTION: COMPOUNDS
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Leydig, Volt & Mayer, Ltd.
: STREET: Two Prudential Plaza, Suite 4900
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/606,143
: FILING DATE: 23-FEB-1996
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Kilyk Jr., John
: REGISTRATION NUMBER: 30763
: REFERENCE/DOCKET NUMBER: 71756
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 616-5600
: TELEFAX: (312) 616-5700
: TELEX: 25-3533
: INFORMATION FOR SEQ ID NO: 26:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 150 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-606-143-26

Query Match          100.0%; Score 85; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 39 DPLRNEYFFDRNRPS 53

RESULT 3
US-08-606-143-29
: Sequence 29, Application US/08606143
: Patent No. 5856155
: GENERAL INFORMATION:
: APPLICANT: LI, MIN
: TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
: TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
: TITLE OF INVENTION: COMPOUNDS
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Leydig, Volt & Mayer, Ltd.
: STREET: Two Prudential Plaza, Suite 4900
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60601
: COMPUTER READABLE FORM:
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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/606,143
: FILING DATE: 23-FEB-1996
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Kilyk Jr., John
: REGISTRATION NUMBER: 30763
: REFERENCE/DOCKET NUMBER: 71756
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 616-5600
: TELEFAX: (312) 616-5700
: TELEX: 25-3533
: INFORMATION FOR SEQ ID NO: 29:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 150 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-606-143-29

Query Match          100.0%; Score 85; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 39 DPLRNEYFFDRNRPS 53

RESULT 4
US-08-606-143-19
: Sequence 19, Application US/08606143
: Patent No. 5856155
: GENERAL INFORMATION:
: APPLICANT: LI, MIN
: TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
: TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
: TITLE OF INVENTION: COMPOUNDS
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Leydig, Volt & Mayer, Ltd.
: STREET: Two Prudential Plaza, Suite 4900
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/606,143
: FILING DATE: 23-FEB-1996
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Kilyk Jr., John
: REGISTRATION NUMBER: 30763
: REFERENCE/DOCKET NUMBER: 71756
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 616-5600
: TELEFAX: (312) 616-5700
: TELEX: 25-3533
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 151 amino acids
: TYPE: amino acid
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-19

Query Match 100.0%; Score 85; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFDRNRPS 15
|||||
DB 39 DPLRNEYFDRNRPS 53

RESULT 5
US-08-606-143-4
Sequence 4, Application US/08606143
Patent No. 5856155

GENERAL INFORMATION:
APPLICANT: LI, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-4

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFDRNRPS 15
|||||
DB 39 DPLRNEYFDRNRPS 53

RESULT 6
US-08-606-143-5
Sequence 5, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:

APPLICANT: LI, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-5

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFDRNRPS 15
|||||
DB 39 DPLRNEYFDRNRPS 53

RESULT 7
US-08-606-143-6
Sequence 6, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: LI, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-6

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRRPS 15
Db 39 DPLRNEYFFDRRPS 53

RESULT 8
US-08-606-143-7
Sequence 7, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-7

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRRPS 15
Db 39 DPLRNEYFFDRRPS 53

RESULT 9
US-08-606-143-9
Sequence 9, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-9

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRRPS 15
Db 39 DPLRNEYFFDRRPS 53

RESULT 10
US-08-606-143-10
Sequence 10, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.

STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-10

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.0e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DPLRNEYFFDRNRPS 15
|
Db 39 DPLRNEYFFDRNRPS 53

RESULT 11
US-08-606-143-12
Sequence 12, Application US/08606143
Patent No. 3856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600

TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-12

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.0e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DPLRNEYFFDRNRPS 15
|
Db 39 DPLRNEYFFDRNRPS 53

RESULT 12
US-08-606-143-13
Sequence 13, Application US/08606143
Patent No. 3856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-13

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.0e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DPLRNEYFFDRNRPS 15
|
Db 39 DPLRNEYFFDRNRPS 53

RESULT 13
US-08-606-143-15
; Sequence 15, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: LI, Min
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ. ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-606-143-15

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFDRNRPS 15
DB 39 DPLRNEYFDRNRPS 53

RESULT 14
US-08-606-143-16
; Sequence 16, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: LI, Min
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ. ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-606-143-16

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFDRNRPS 15
DB 39 DPLRNEYFDRNRPS 53

RESULT 15
US-08-606-143-18
; Sequence 18, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: LI, Min
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ. ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-606-143-18

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DPLRNEYFFDRNRPS 15
|||
Db 39 DPLRNEYFFDRNRPS 53

Search completed: February 2, 2001, 10:36:29
Job time: 42 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 2, 2001, 10:38:00 ; Search time 45.64 Seconds
(without alignments)
11.238 Million cell updates/sec

Title: US-09-273-217-2
Perfect score: 85
Sequence: 1 DPLRNEYFFDRNRPS 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues
Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.GeneSeq.36:*

- 1: /SIDSL/gcgdata/geneSeq/geneSeq/AA1980.DAT:*
- 2: /SIDSL/gcgdata/geneSeq/geneSeq/AA1981.DAT:*
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- 5: /SIDSL/gcgdata/geneSeq/geneSeq/AA1984.DAT:*
- 6: /SIDSL/gcgdata/geneSeq/geneSeq/AA1985.DAT:*
- 7: /SIDSL/gcgdata/geneSeq/geneSeq/AA1986.DAT:*
- 8: /SIDSL/gcgdata/geneSeq/geneSeq/AA1987.DAT:*
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- 13: /SIDSL/gcgdata/geneSeq/geneSeq/AA1992.DAT:*
- 14: /SIDSL/gcgdata/geneSeq/geneSeq/AA1993.DAT:*
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- 20: /SIDSL/gcgdata/geneSeq/geneSeq/AA1999.DAT:*
- 21: /SIDSL/gcgdata/geneSeq/geneSeq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	Y42763	Rat potassium chan
2	85	100.0	495	20	Human cation chann
3	80	94.1	616	Y32014	Drosophila melanog
4	58	68.2	532	16	Mouse Kv1.7 volta
5	57	67.1	556	20	Caenorhabditis ele
6	49	57.6	499	20	Human potassium ch
7	43	50.6	513	17	Human K+ channel 1
8	43	50.6	513	19	Putative mature po
9	42	49.4	858	20	Human cation chann
10	41	48.2	477	20	Human potassium ch
11	40	47.1	157	20	Human Kv6.2 protei
12	40	47.1	466	20	Human Kv6.2 protei

13	40	47.1	494	17	R90765
14	40	47.1	494	19	M42996
15	40	47.1	495	20	Y33766
16	39	45.9	491	21	Y70454
17	38.5	45.3	490	20	Y34121
18	38.5	45.3	491	21	Y53780
19	37.5	44.1	506	21	Y44564
20	37.5	44.1	506	21	Y44566
21	37.5	44.1	506	21	Y44567
22	37.5	44.1	506	21	Y44568
23	37	43.5	457	20	W87970
24	37	43.5	635	20	Y24321
25	37	43.5	663	20	Y24332
26	37	43.5	680	20	Y24330
27	37	43.5	811	17	R95014
28	37	43.5	812	17	R95017
29	37	43.5	841	20	Y24318
30	37	43.5	862	20	W87971
31	37	43.5	1477	16	R67691
32	37	43.5	1477	18	W10424
33	37	43.5	1477	20	Y06819
34	37	43.5	2710	17	R95016
35	37	43.5	2710	19	W68387
36	36	42.4	35	16	R77937
37	36	42.4	35	18	M46130
38	36	42.4	35	19	W53080
39	36	42.4	35	21	Y51735
40	36	42.4	35	21	Y80432
41	36	42.4	48	19	W79087
42	36	42.4	90	21	Y64651
43	36	42.4	214	20	Y13524
44	36	42.4	256	20	Y34125
45	36	42.4	257	21	Y70452

ALIGNMENTS

RESULT 1

Y42763 standard; peptide: 15 AA.

Y42763:

20-DEC-1999 (first entry)

Rat potassium channel Kv1.2 intracellular N-terminal peptide #2.

Ion channel; potassium channel; vestibule; inhibitor; antibody;

polycation; antagonist; hypertension; cardiac ischemia;

bronchial constriction; neurological diseases.

Synthetic.

Rattus sp.

W09948927-A1.

30-SEP-1999.

19-MAR-1999; 99WO-US06019.

25-MAR-1998; 98US-0079268.

(CORR) CORNELL RES FOUND INC.

Huang X;

WPI: 1999-601205/51.

Designing specific blockers that bind to the external vestibule region

of ion channels, potentially useful for treating e.g. hypertension -

Example 3; Page 13; 40pp; English.

XX This sequence represents a peptide (#2), derived from the intracellular
CC N-terminus of the rat delayed rectifier potassium channel Kv1.2.
CC This was conjugated to keyhole limpet haemocyanin (KLH) and used to
CC generate polyclonal antibodies. These antibodies were used as a control
CC in studies of potassium channel inhibition by antibodies raised against
CC the extracellular vestibule-derived peptides #1 (Y4261), #3
CC (Y4263) and #4 (Y4276). The vestibule portion of potassium
CC channels is located on the extracellular portion of the channel protein,
CC and generally comprises a loop between the S5 transmembrane domain and
CC the pore forming region of the channel, or between the pore forming
CC region and the S6 transmembrane domain. Antibodies generated against
CC vestibule peptides act as potassium channel inhibitors by binding to the
CC vestibule portion, physically blocking the pore, or otherwise inducing a
CC conformational change in the channel. These potassium channel blockers
CC are potential therapeutic agents for e.g., hypertension, cardiac
CC ischaemia, bronchial constriction and neurological diseases. Such
CC inhibitors are specific for particular types of ion channel, and
CC are produced by rational design based on known nucleotide and amino acid
CC sequences for ion channels.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 85; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.3e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFEDRRPS 15
ID Y32014
DB 1 dplrneyfdrnps 15

RESULT 2
Y32014
ID Y32014 standard; Protein; 495 AA.

XX Y32014;
AC
XX
XX
DT 05-JAN-2000 (first entry)
XX

DE Human cation channel protein.

XX Cation channel protein; CCP; ion transport; arrhythmia;
KW diabetes mellitus; seizure; asthma; hypertension; therapy;
KM protein engineering; human.
XX
OS Homo sapiens.

XX
XX
FH Key

FT Location/Qualifiers
FT Region 61..119
FT /note="crystal region"
XX
PN WO9947923-A2.

XX
XX
PD 23-SEP-1999.
XX

PF 22-MAR-1999; 99MO-US06307.

XX
XX
PR 20-MAR-1998; 98US-0045529.
PR 02-APR-1998; 98US-0054347.

XX (UYRQ) UNIV ROCKEFELLER.

XX
XX
PI Macklinon R;
XX

DR WPI; 1999-601131/51.

XX Assays for screening compounds which interact with cation channel
PT proteins, useful for providing agents for treatment of diseases -
XX
XX Claim 21; Page 135-137; 165pp: English.
PS
XX

CC The present sequence represents a human cation channel protein
CC (CCP). The invention provides an assay for screening potential
CC drugs or agents which interact with CCPs using prokaryotic CCPs
CC (such as those given in Y32009-12) mutated, using recombinant DNA
CC technology, to mimic the physiological function and chemical
CC properties of a functional eukaryotic CCP (such as those given in
CC Y32013-22). An example of a mutated prokaryotic CCP is given in
CC Y32024. The crystal region of the CCP may also be used in the
CC assay. The drugs or agents obtained can be used to treat
CC conditions related to the function of CCP in vivo, such as cardiac
CC arrhythmia, diabetes mellitus, seizure disorder, asthma or
CC hypertension. The invention has overcome the physical limitations
CC regarding the isolation and purification of eukaryotic CCPs.
XX
SQ Sequence 495 AA;

Query Match 100.0%; Score 85; DB 20; Length 495;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFEDRRPS 15
ID Y32013
DB 74 dplrneyfdrnps 88

RESULT 3
Y32013
ID Y32013 standard; Protein; 616 AA.

XX Y32013;
AC
XX
XX
DT 05-JAN-2000 (first entry)
XX

DE Drosophila melanogaster cation channel protein.

XX Cation channel protein; CCP; ion transport; arrhythmia;
KW diabetes mellitus; seizure; asthma; hypertension; therapy;
KM protein engineering.
XX
OS Drosophila melanogaster.

XX
XX
FH Key

FT Location/Qualifiers
FT Region 61..119
FT /note="crystal region"
XX
PN WO9947923-A2.

XX
XX
PD 23-SEP-1999.
XX

PF 22-MAR-1999; 99MO-US06307.

XX
XX
PR 20-MAR-1998; 98US-0045529.
PR 02-APR-1998; 98US-0054347.

XX (UYRQ) UNIV ROCKEFELLER.

XX
XX
PI Macklinon R;
XX

DR WPI; 1999-601131/51.

XX Assays for screening compounds which interact with cation channel
PT proteins, useful for providing agents for treatment of diseases -
XX
XX Claim 21; Page 133-135; 165pp: English.
PS

XX The present sequence represents a Drosophila melanogaster cation
CC channel protein (CCP). The invention provides an assay for
CC screening potential drugs or agents which interact with CCPs using
CC prokaryotic CCPs (such as those given in Y32009-12) mutated, using
CC recombinant DNA technology, to mimic the physiological function and
CC chemical properties of a functional eukaryotic CCP (such as those
CC given in Y32013-22). An example of a mutated prokaryotic CCP is

CC given in Y32013-22). An example of a mutated prokaryotic CCP is
 CC given in Y32024. The crystal region of the CCP may also be used in
 CC the assay. The drugs or agents obtained can be used to treat
 CC conditions related to the function of CCP in vivo, such as cardiac
 CC arrhythmia, diabetes mellitus, seizure disorder, asthma or
 CC hypertension. The invention has overcome the physical limitations
 CC regarding the isolation and purification of eukaryotic CCPs.

XX Sequence 556 AA;

Query Match 67.1%; Score 57; DB 20; Length 556;
 Best Local Similarity 83.3%; Pred. No. 0.037;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRN 12
 ||| |||||
 Db 72 dplneyffdrn 83

RESULT 6
 Y34122
 ID Y34122 standard; Protein; 499 AA.

XX Y34122;
 XX 30-NOV-1999 (first entry)

XX Human potassium channel K+hov9.

XX Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
 XX cardiovascular disorder; CNS disorder; renal disorder.

XX Homo sapiens.

XX MO9943696-A1.

XX 02-SEP-1999.

XX 22-FEB-1999; 99WO-US03826.

XX 19-JAN-1999; 99US-0116448.

XX 25-FEB-1998; 98US-0076887.

XX 07-AUG-1998; 98US-0095836.

XX (AXYS-) AXYS PHARM INC.

XX Curran ME, Hu P, Miller AP, Rutter M, Wang J;

XX WPI; 1999-527591/44.

XX N-PSDB; 211900.

XX New nucleic acids encoding mammalian K+hov potassium channel
 PT proteins, useful for the diagnosis and treatment of episodic ataxia
 PT with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome
 XX Claim 3; Page 56-57; 112pp; English.

XX This sequence represents the human K+hov9 potassium channel.
 CC K+hov proteins have a high degree of homology to known potassium
 CC channels and may be alpha subunits, which form the functional channel,
 CC or accessory subunits that act to modulate the channel activity.
 CC K+hov9 is a voltage gated potassium channel. The gene's
 CC chromosomal location is 8q23, determined via PCR chromosomal
 CC localization using primers 211922 and 211923. K+hov9 cDNAs were
 CC isolated by extension of expressed sequence tags (ESTs) which were
 CC related but not identical to known human potassium channels. Potential
 CC polymorphisms detected as sequence variants between multiple
 CC independent clones. Potassium channels have critical roles in various
 CC cell types and biochemical pathways. Defective potassium channels are
 CC known to cause four human diseases: episodic ataxia with myokymia;
 CC cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
 CC As potassium channels are critical components of virtually all cells,

CC It is likely that abnormal potassium channels are also implicated in
 CC certain renal, cardiovascular and central nervous system (CNS) disorders.
 CC Nucleotides encoding K+hov proteins may be used for identifying
 CC homologous or related proteins and the DNA sequences encoding them. They
 CC may be used to produce compositions that modulate the expression and
 CC function of the K+hov protein and in studying the biochemical pathways
 CC associated with it. They may also be used for the recombinant production
 CC of K+hov protein in fermentation cultures. Additionally, such
 CC nucleotides may be used in gene therapy protocols for the treatment
 CC of diseases associated with abnormal potassium channels.

XX Sequence 499 AA;

Query Match 57.6%; Score 49; DB 20; Length 499;
 Best Local Similarity 66.7%; Pred. No. 0.82;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRN 12
 ||| |||||
 Db 95 npvdneffdrn 106

RESULT 7
 R90764
 ID R90764 standard; Protein; 513 AA.

XX R90764;

XX 25-APR-1996 (first entry)

XX Human K+ channel 1 mature protein.

XX Potassium channel; K+ channel 1; K+ channel 2; agonist; antagonist;
 XX hypertension; cancer.

XX Homo sapiens.

XX MO9603415-A1.

XX 08-FEB-1996.

XX 28-JUL-1994; 94WO-US08449.

XX 28-JUL-1994; 94WO-US08449.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Adams MD, Li Y, White OR;

XX WPI; 1996-116983/12.

XX N-PSDB; T12461.

XX Human potassium channel 1 and 2 proteins - also their agonists and
 PT antagonists, useful to treat e.g. hypertension or cancer,
 PT respectively
 XX Claim 15; Page 39-41; 63pp; English.

XX 2 cDNA sequences (T12461-62) isolated from a human brain cDNA
 CC library code for K+ channel 1 (R90764) and K+ channel 2 (R90765),
 CC respectively. The proteins may be obtained by expression of the
 CC cDNAs in e.g. insect Sf9 or mammal COS cells. They can be used
 CC to screen potential agonists useful for treating hypertension,
 CC epilepsy, stroke, asthma, Parkinson disease, schizophrenia,
 CC anxiety, depression and neurodegeneration, and antagonists useful
 CC to treat migraine, autoimmune disease, cancer and graft rejection,
 CC or to raise diagnostic antibodies.

XX Sequence 513 AA;

Query Match 50.6%; Score 43; DB 17; Length 513;

Best Local Similarity 87.5%; Pred. No. 9.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 NEFFDRN 12
|:|||||
DB 113 neffdrn 120

RESULT 8

W42995
ID W42995 standard; Protein; 513 AA.

AC W42995;

DT 30-APR-1998 (first entry)

DE Putative mature potassium channel 1 protein.

KM Potassium channel 1 protein; K⁺ channel; cellular homeostasis;
agonist; antagonist.

OS Homo sapiens.

PN US5710019-A.

PD 20-JAN-1998.

PF 05-JUN-1995; 95US-0464340.

PR 05-JUN-1995; 95US-0464340.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Adams MD, Li Y, White OR;

DR WPI; 1998-109815/10.

DR N-PSDB; V04873.

PT Potassium channel polypeptides and their agonists - useful for
treating e.g. epilepsy, stroke, hypertension and asthma also for

PT antibody production

PS Claim 3; Fig 1A-C; 35pp; English.

CC The present sequence represents a putative mature potassium (K⁺) channel 1
protein. The cDNA sequence was isolated from a cDNA library derived

CC from brain tissue. It is structurally related to the K⁺ channel gene
family. K⁺ channels are involved in normal cellular homeostasis and are

CC associated with a variety of disease states and immune responses.

CC The proteins can be used to produce antibodies for use in screening
assays for agonists or antagonists of K⁺ channel proteins. Agonists of

CC the polypeptides can be used in methods for treating hypertension,
epilepsy, stroke, asthma, Parkinson's disease, schizophrenia, anxiety,

CC depression and neurodegeneration. Antagonists of the polypeptides are
used for treating migraine, autoimmune diseases, cancer and graft

CC rejection.

CC

SQ Sequence 513 AA:

Query Match 50.6%; Score 43; DB 19; Length 513;
Best Local Similarity 87.5%; Pred. No. 9.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 NEFFDRN 12
|:|||||
DB 113 neffdrn 120

RESULT 9

Y32015
ID Y32015 standard; Protein; 858 AA.

XX

AC Y32015;

DT 05-JAN-2000 (first entry)

DE Human cation channel protein.

KM Cation channel protein; CCP; ion transport; arrhythmia;
diabetes mellitus; seizure; asthma; hypertension; therapy;

KM protein engineering; human.

OS Homo sapiens.

FT Key Location/Qualifiers
Region 61..119
/note="crystal region"

FT

PN W09947923-A2.

PD 23-SEP-1999.

PF 22-MAR-1999; 99WO-US06307.

PR 20-MAR-1998; 98US-0045529.

PR 02-APR-1998; 98US-0054347.

PA (UYRO) UNIV ROCKEFELLER.

PI Mackinnon R;

DR WPI; 1999-601131/51.

PT Assays for screening compounds which interact with cation channel
proteins, useful for providing agents for treatment of diseases -

PS Claim 21; Page 137-140; 165pp; English.

XX

CC The present sequence represents a human cation channel protein
(CCP). The invention provides an assay for screening potential

CC drugs or agents which interact with CCPs using prokaryotic CCPs
(such as those given in Y32009-12) mutated, using recombinant DNA

CC technology, to mimic the physiological function and chemical
properties of a functional eukaryotic CCP (such as those given in

CC Y32013-22). An example of a mutated prokaryotic CCP is given in
Y32024. The crystal region of the CCP may also be used in the

CC assay. The drugs or agents obtained can be used to treat
conditions related to the function of CCP in vivo, such as cardiac

CC arrhythmia, diabetes mellitus, seizure disorder, asthma or
hypertension. The invention has overcome the physical limitations

CC regarding the isolation and purification of eukaryotic CCPs.

XX

SQ

Sequence 858 AA:

Query Match 49.4%; Score 42; DB 20; Length 858;
Best Local Similarity 87.5%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 NEFFDRN 12
|:|||||
DB 81 neffdrn 88

RESULT 10
Y34127
ID Y34127 standard; Protein; 477 AA.

AC Y34127;

DT 30-NOV-1999 (first entry)

DE Human potassium channel K⁺hnav11.
Potassium channel; ataxia; arrhythmia; epilepsy; Barter's syndrome;

KW		cardiovascular disorder; CNS disorder; renal disorder.
XX		
OS	Homo sapiens.	
PN	MO9943696-A1.	
XX		
PD	02-SEP-1999.	
XX		
PF	22-FEB-1999;	99WO-US03826.
XX		
PR	19-JAN-1999;	99US-0116448.
PR	25-FEB-1998;	98US-0076687.
PR	07-AUG-1998;	98US-0095836.
PA	(AAXS-) AAXS PHARM INC.	
XX		
P1	Curran ME, Hu P, Miller AP, Rutter M, Wang J;	
DR	WPI: 1999-527591/44.	
N-PSDB:	Z11903.	
PT	New nucleic acids encoding mammalian K+Hnov potassium channel proteins, useful for the diagnosis and treatment of episodic ataxia with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome	
PS	Claim 3; Page 71-72; 112pp; English.	
CC	This sequence represents the human K+Hnov1 potassium channel.	
CC	K+Hnov proteins have a high degree of homology to known potassium channels and may be alpha subunits, which form the functional channel, or accessory subunits that act to modulate the channel activity. K+Hnov1 is a 6 transmembrane domain, voltage gated, delayed rectifier potassium channel. K+Hnov cDNAs were isolated by extension of expressed sequence tags (ESTs) which were related but not identical to known human potassium channels. Potential polymorphisms detected as sequence variants between multiple independent clones. Potassium channels have critical roles in various cell types and biochemical pathways. Defective potassium channels are known to cause four human diseases: episodic ataxia with myokymia; cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium channels are critical components of virtually all cells, it is likely that abnormal potassium channels are also implicated in certain renal, cardiovascular and central nervous system (CNS) disorders. Nucleotides encoding K+Hnov proteins may be used for identifying homologous or related proteins and the DNA sequences encoding them. They may be used to produce compositions that modulate the expression and function of the K+Hnov protein and in studying the biochemical pathways associated with it. They may also be used for the recombinant production of K+Hnov protein in fermentation cultures. Additionally, such nucleotides may be used in gene therapy protocols for the treatment of diseases associated with abnormal potassium channels.	
SQ	Sequence	477 AA;
OY	1 DPLRNEYFFDRN 12	
D6	63 davgreyfdn 74	
RESULT	11	
Y50343	standard; Protein: 157 AA.	
AC	Y50343;	
DT	18-JAN-2000 (first entry)	
DE	Human Kv6.2 protein fragment.	
XX		

KW	Kv6.2; potassium channel protein Kv2.1; myocardium; hippocampus; stroke;
KM	propafenone; voltage-dependent potassium channel; therapy; treatment;
KW	class IC anti-arrhythmic; cardiovascular disease; nervous system disease;
KM	antihypertensive; cardioprotectant; learning disorder; memory disorder;
KV	neurodegenerative disorder; epilepsy; ischemia; Parkinson's disease;
KX	Alzheimer's disease.
XX	
OS	Homo sapiens.
XX	
PN	DEJ9841413-C1.
XX	
PD	23-SEP-1999.
XX	
PF	06-AUG-1998; 98DE-1041413.
XX	
PR	06-AUG-1998; 98DE-1041413.
XX	
PA	(GENT-) FORSCHUNGSGESELLSCHAFT GENTON MBH.
XX	
PI	Netzer R, Pongs O;
XX	
DR	WPL: 1999-519712/44.
DR	N-PSD: 223805.
XX	
PT	New potassium channel protein, Kv6.2, used to screen for specific
PS	modulators, potentially useful e.g. as antiarrhythmic agents -
XX	
PS	Disclosure; Page 20; 42pp; German.
CC	
CC	This invention describes a novel potassium channel protein (I) Kv6.2.
CC	This protein forms, with the protein Kv2.1, voltage-dependent potassium
CC	channels that are expressed preferentially in the myocardium and
CC	hippocampus and have high affinity for propafenone. The channels are used
CC	to identify specific modulators which are potentially useful as
CC	therapeutic agents, particularly as class IC anti-arrhythmics, but more
CC	generally agents for treating cardiovascular or nervous system diseases,
CC	e.g. anti-hypertensives or cardioprotectants, or for treating learning and
CC	memory disorders or neurodegenerative disorders such as epilepsy,
CC	ischemia, stroke, or Parkinson's or Alzheimer's diseases. Nucleic acid
CC	that encodes (I) is used for recombinant production of (I), particularly
CC	to generate cells for drug screening. (I) is also used to raise specific
CC	antibodies. This sequence represents a fragment of the human Kv6.2
CC	protein described in the method of the invention.
XX	
SQ	Sequence 157 AA;
QY	
Db	
QY	1 DPLRNEVFEDRN 12
	1:1:
	1:1:
	63 dvsrdefldrs 74
ID	
RESULT 12	
Y50341	
ID	Y50341 standard; Protein; 466 AA.
XX	
AC	Y50341;
XX	
DT	18-JAN-2000 (first entry)
XX	
DE	Human Kv6.2 protein.
XX	
KM	Kv6.2; potassium channel protein; Kv2.1; myocardium; hippocampus; stroke;
KM	propafenone; voltage-dependent potassium channel; therapy; treatment;
KW	class IC anti-arrhythmic; cardiovascular disease; nervous system disease;
KM	anti-hypertensive; cardioprotectant; learning disorder; memory disorder;
KV	neurodegenerative disorder; epilepsy; ischemia; Parkinson's disease;
KX	Alzheimer's disease.
XX	

OS Homo sapiens.
 XX DE19841413-C1.
 XX 23-SEP-1999.
 XX
 XX PF 06-AUG-1998; 98DE-1041413.
 XX PR 06-AUG-1998; 98DE-1041413.
 XX
 XX (GENI-) FORSCHUNGSGESELLSCHAFT GENION MBH.
 XX
 PI Netzer R, Pongs O;
 XX WPI: 1999-519712/44.
 DR N-PSDB: Z23803.
 XX
 PT New potassium channel protein, Kv6.2, used to screen for specific
 PT modulators, potentially useful e.g. as antiarrhythmic agents -
 XX
 PS Claim 1; Page 13-15; 42pp; German.
 XX
 CC This invention describes a novel potassium channel protein (I) Kv6.2.
 CC This protein forms, with the protein Kv2.1, voltage-dependent potassium
 CC channels that are expressed preferentially in the myocardium and
 CC hippocampus and have high affinity for propafenone. The channels are used
 CC to identify specific modulators which are potentially useful as
 CC therapeutic agents, particularly as class IC anti-arrhythmics, but more
 CC generally agents for treating cardiovascular or nervous system diseases,
 CC e.g. antihypertensives or cardioprotectants, or for treating learning and
 CC memory disorders or neurodegenerative disorders such as epilepsy,
 CC ischemia, stroke, or Parkinson's or Alzheimer's diseases. Nucleic acid
 CC that encodes (I) is used for recombinant production of (I), particularly
 CC to generate cells for drug screening. (I) is also used to raise specific
 CC antibodies. This sequence represents the human Kv6.2 protein described in
 CC the method of the invention.
 CC
 SQ Sequence 466 AA;

Query Match 47.1%; Score 40; DB 20; Length 466;
 Best Local Similarity 58.3%; Pred. No. 28;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRN 12
 | 1:1:|||||:
 Db 63 dvrdeffdr 74

RESULT 13
 R90765 ID R90765 standard; Protein; 494 AA.
 XX
 AC R90765;
 XX
 DT 25-APR-1996 (first entry)
 XX
 DE Human K+ channel 2 mature protein.
 XX
 KW Potassium channel; K+ channel 1; K+ channel 2; agonist; antagonist;
 KW hypertension; cancer.
 XX
 OS Homo sapiens.
 OS
 PN WO9603415-A1.
 XX
 PD 08-FEB-1996.
 XX
 PF 28-JUL-1994; 94WO-US08449.
 XX
 PR 28-JUL-1994; 94WO-US08449.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.

XX
 PI Adams MD, Li Y, White OR.
 XX WPI: 1996-116983/12.
 DR N-PSDB: T12462.
 XX
 PT Human potassium channel 1 and 2 proteins - also their agonists and
 PT antagonists, useful to treat e.g. hypertension or cancer.
 PT respectively
 XX
 PS Claim 15; Page 43-45; 63pp; English.
 XX
 CC 2 cDNA sequences (T12461-62) isolated from a human brain cDNA
 CC library code for K+ channel 1 (R90764) and K+ channel 2 (R90765),
 CC respectively. The proteins may be obt'd. by expression of the
 CC cDNAs in e.g. insect Sf9 or mammal COS cells. They can be used
 CC to screen potential agonists useful for treating hypertension,
 CC epilepsy, stroke, asthma, Parkinson disease, schizophrenia,
 CC anxiety, depression and neurodegeneration, and antagonists useful
 CC to treat migraine, autoimmune disease, cancer and graft rejection,
 CC or to raise diagnostic antibodies.
 CC
 SQ Sequence 494 AA;

Query Match 47.1%; Score 40; DB 17; Length 494;
 Best Local Similarity 50.0%; Pred. No. 30;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRN 12
 | 1:1:|||||:
 Db 71 dpgkreydrd 82

RESULT 14
 W42996 ID W42996 standard; Protein; 494 AA.
 XX
 AC W42996;
 XX
 DT 30-APR-1998 (first entry)
 XX
 DE Putative mature potassium channel 2 protein.
 XX
 KW Potassium channel 2 protein; K+ channel; cellular homeostasis;
 KW agonist; antagonist.
 XX
 OS Homo sapiens.
 OS
 PN US5710019-A.
 XX
 PD 20-JAN-1998.
 XX
 PF 05-JUN-1995; 95US-0464340.
 XX
 PR 05-JUN-1995; 95US-0464340.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Adams MD, Li Y, White OR.
 XX
 DR WPI: 1998-109815/10.
 DR N-PSDB: Y04874.
 XX
 PT Potassium channel polypeptides and their agonists - useful for
 PT treating e.g. epilepsy, stroke, hypertension and asthma also for
 PT antibody production
 XX
 PS Claim 4; Fig 2A-E; 35pp; English.
 XX
 CC The present sequence represents a putative mature potassium (K+) channel 2
 CC protein. The cDNA sequence was isolated from a cDNA library derived
 CC from brain tissue. It is structurally related to the K+ channel gene

CC family. K+ channels are involved in normal cellular homeostasis and are
 CC associated with a variety of disease states and immune responses.
 CC The proteins can be used to produce antibodies for use in screening
 CC assays for agonists or antagonists of K+ channel proteins. Agonists of
 CC the polypeptides can be used in methods for treating hypertension,
 CC epilepsy, stroke, asthma, Parkinson's disease, schizophrenia, anxiety,
 CC depression and neurodegeneration. Antagonists of the polypeptides are
 CC used for treating migraine, autoimmune diseases, cancer and graft
 CC rejection.

SO Sequence 494 AA;

Query Match 47.1%; Score 40; DB 19; Length 494;
 Best Local Similarity 50.0%; Pred. No. 30;

Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRN 12
 11 : 1 : 1111 :
 Db 71 dpqkrefyfd 82

RESULT 15

ID Y33766 standard; Protein; 495 AA.

AC Y33766;

DT 09-NOV-1999 (first entry)

DE hkv5.1 human brain-specific potassium channel.

KW Potassium channel; brain; hkv1.5; epilepsy; Alzheimer's disease;

KM synaptic transmission; electrical excitability; anxiety;

KM schizophrenia; Parkinson's disease; mental retardation; asthma;

OS Homo sapiens.

PN MO9941372-A1.

PD 19-AUG-1999.

PF 11-FEB-1999; 99WO-GB00423.

PR 17-FEB-1998; 98US-0074999.

PA (ZENE) ZENCA LTD.

PI Aiyar J, Logsdon NJ, Zhou J;

DR WPI; 1999-527368/44.

DR N-PSDB; 206652, 206653.

PT New polynucleotide encoding the potassium channel modulatory subunit
 PT human hkv5.1, used to identify modulators used to treat, prevent or
 PT diagnose e.g. epilepsy or Alzheimer's disease
 PS Claim 1; Page 92-93; 110pp; English.

CC This sequence is the human brain specific potassium channel hkv5.1
 CC polypeptide. hkv5.1 is a neuronal modulatory subunit involved in
 CC regulating synaptic transmission and electrical excitability in the
 CC brain. The hkv5.1 polypeptide can be used to identify modulators of its
 CC activity; to raise specific antibodies and to purify effectors from
 CC natural sources. Sequences antisense to hkv5.1 are useful for diagnosis,
 CC treatment, study and prevention of diseases mediated by potassium channel
 CC activity in the brain and associated with dysfunctional neurons. These
 CC diseases are cognitive, behavioural, psychological, neurodegenerative or
 CC developmental, e.g. anxiety, schizophrenia, Alzheimer's or Parkinson's
 CC diseases, mental retardation, asthma, migraine, epilepsy and stroke.
 CC Particular applications are treatment of epilepsy or Alzheimer's disease.
 CC Antibodies against hkv5.1 are used as therapeutic modulators; for

CC diagnostic measurement of hkv5.1 levels and for purification of hkv5.1 by
 CC affinity chromatography.

SO Sequence 495 AA;

Query Match 47.1%; Score 40; DB 20; Length 495;
 Best Local Similarity 50.0%; Pred. No. 30;

Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRN 12
 11 : 1 : 1111 :
 Db 72 dpqkrefyfd 83

Search completed: February 2, 2001, 10:38:02
 Job Time: 135 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 2, 2001, 10:41:47 ; Search time 20.39 Seconds
(without alignments)
22.173 Million cell updates/sec

Title: US-09-273-217-3
Perfect score: 79
Sequence: 1 GAOPNDPSASEH 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	511	1	CIKD_HUMAN
2	79	100.0	511	2	CIKD_MOUSE
3	79	100.0	585	1	CIKD_RAT
4	71	89.9	638	1	CIKE_RAT
5	47	59.5	354	1	CAHC_HUMAN
6	47	59.5	582	1	CIKG_HUMAN
7	47	59.5	625	1	CIKG_RAT
8	44	55.7	2327	1	CCAB_MOUSE
9	44	55.7	2336	1	CCAB_RAT
10	42	53.2	1435	1	Y194_HUMAN
11	39	49.4	716	1	DVL3_HUMAN
12	39	49.4	716	1	DVL3_MOUSE
13	39	49.4	1060	1	UAY_EMR1
14	39	49.4	1136	1	CABA_BACTI
15	39	49.4	2869	1	RBPL_PLAIV
16	38	48.1	386	1	PSD4_ARATH
17	38	48.1	513	1	PPT1_YEAST
18	38	48.1	602	1	EIL_MOUSE
19	38	48.1	603	1	BPRV_BACNO
20	38	48.1	727	1	CCT1_HORSE
21	38	48.1	757	1	CIKE_HUMAN
22	38	48.1	769	1	CIKE_MOUSE
23	38	48.1	798	1	HMPB_DROME
24	38	48.1	889	1	CIKE_RAT
25	38	48.1	1841	1	CC12_SCHPO
26	38	48.1	2052	1	YDOB_SCHPO
27	37	46.8	181	1	CEN_ANTMA
28	37	46.8	215	1	YCK1_YEAST
29	37	46.8	350	1	NTRB_VITBAL
30	37	46.8	432	1	YISA_YEAST
31	37	46.8	469	1	GLNA_AQUAE
32	37	46.8	561	1	VAT7_SCHPO
33	37	46.8	793	1	CLPA_RHOBL

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	511 AA.
CIKD_HUMAN				
ID	CIKD_HUMAN			
AC	P48547			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.1 (KV4) (NGK2).			
GN	KCNK1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OC	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93194190; PubMed=8449507;			
RA	Ried T., Rudy B., de Miera E., Lau D., Ward D.C., Sen K.;			
RT	"Localization of a highly conserved human potassium channel gene			
RL	(NGK2-KV4; KCNC1) to chromosome 11p15.";			
RL	Genomics 15:405-411(1993).			
RL	[2]			
RP	SEQUENCE OF 244-475 FROM N.A.			
RX	MEDLINE=93016011; PubMed=1400413;			
RA	Grismer S., Ganshanti S., Dethlefs B., McPherson J.D.,			
RT	Wasmuth J.J., Gutman G.A., Cahalan M.D., Chandy K.G.;			
RL	"The Shaw-related potassium channel gene, Kv3.1, on human chromosome			
RL	11, encodes the type 1 K+ channel in T cells.";			
RL	J. Biol. Chem. 267:20971-20979(1992).			
CC	- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM			
CC	ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED			
CC	CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE			
CC	MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH			
CC	WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL			
CC	GRADIENT.			
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS			
CC	CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT			
CC	EVERY THIRD POSITION.			
CC	- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL			
CC	ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR			
CC	COMPARTMENTS.			
CC	- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER			
CC	CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; S56770; AAB25764.1; -			P17393 hepatitis b
DR	EMBL; M96747; AAA59458.1; -			P31380 saccharomyc
DR	MIM; 176258; -			Q24167 dtosophila
DR	INTERPRO; IPR000636; -			Q07157 homo sapien
DR	INTERPRO; IPR003091; -			P51572 homo sapien
				P09272 varicella-z
				O90346 cyprius ca
				Q92428 mus musculu
				P38142 saccharomyc
				P35974 measles vir
				P03422 measles vir
				P26033 measles vir

```

DR PFAM: PF00520: Ion.trans; 1.
CC PRINTS: PR00169: KCHANNEL.
CC Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Glycoprotein; Multigene family.
KW DOMAIN 1 190
FT TRANSSEM 191 209 SEGMENT S1 (POTENTIAL).
FT DOMAIN 210 247 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 248 267 SEGMENT S2 (POTENTIAL).
FT DOMAIN 268 276 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 277 295 SEGMENT S3 (POTENTIAL).
FT DOMAIN 296 308 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 309 331 SEGMENT S4 (POTENTIAL).
FT DOMAIN 332 344 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 345 366 SEGMENT S5 (POTENTIAL).
FT DOMAIN 367 414 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 415 436 SEGMENT S6 (POTENTIAL).
FT DOMAIN 437 511 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 511 AA: 57942 MW: 10A93478F7120ABB CRC64;

Query Match 100.0%; Score 79; DB 1; Length 511;
Best Local Similarity 100.0%; Pred. No. 9.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAOPNDPASEBTH 14
Db 370 GAOPNDPASEBTH 383
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CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/
CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL: Y07521: CAA68814.1; -.
DR PIR: S07095: S07095.
DR MGD: MGI:96667: KCNC1.
DR INTERPRO: IPR000636: -.
DR INTERPRO: IPR003091: -.
DR PFAM: PF00520: Ion.trans; 1.
DR PRINTS: PR00169: KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Glycoprotein; Multigene family; Alternative splicing.
FT DOMAIN 1 190
FT TRANSSEM 191 209 SEGMENT S1 (POTENTIAL).
FT DOMAIN 210 247 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 248 267 SEGMENT S2 (POTENTIAL).
FT DOMAIN 268 276 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 277 295 SEGMENT S3 (POTENTIAL).
FT DOMAIN 296 308 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 309 331 SEGMENT S4 (POTENTIAL).
FT DOMAIN 332 344 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 345 366 SEGMENT S5 (POTENTIAL).
FT DOMAIN 367 414 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 415 436 SEGMENT S6 (POTENTIAL).
FT DOMAIN 437 511 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 511 AA: 57928 MW: 50A939E8F7120E37 CRC64;

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Query Match 100.0%; Score 79; DB 1; Length 511;
Best Local Similarity 100.0%; Pred. No. 9.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GAOPNDPASEBTH 14
Db 370 GAOPNDPASEBTH 383
|||||

RESULT 3
CIRD_RAT
ID CIRD_RAT STANDARD; PRT; 585 AA.
AC P25122;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.1 (KV4) (NGK2) (RAW2).
GN KCNC1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91219486; PubMed-2023941;
RA Luneau C.J., Williams J.B., Marshall J., Levitan E.S., Oliva C.,
RA Smith J.S., Antanavage J., Folander K., Steln R.B., Swanson R.,
RA Kaczmarek L.K., Bubrow S.A.;
RT "Alternative splicing contributes to K+ channel diversity in the
RT mammalian central nervous system."
RT Proc. Natl. Acad. Sci. U.S.A. 88:3932-3936(1991).
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-92331599; PubMed-1378392;
RA Rettig J., Wunder F., Stocker M., Lichtinghagen R., Mastiaux F.,
RA Beckh S., Kues W., Pedarzani P., Schroeter K.H., Ruppersberg J.P.,
RA Voh R., Pongs O.;
RT "Characterization of a Shaw-related potassium channel family in rat
RT brain."
RL EMBL J. 11:2473-2486(1992).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE

```

MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE SPLICING.

-1- TISSUE SPECIFICITY: BRAIN.

-1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

-1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.

-1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.

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EMBL: M68880; AAA41501.1; -

EMBL: X62840; CAA4464.1; -

PIR: A39395; A39395.

PIR: S22704; S22704.

INTERPRO: IPR000636; -

DR INTERPRO: IPR003091; -

DR PFAM: PF00520; Ion.trans. 1.

DR PRINTS: PR00169; KCHANNEL.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Glycoprotein; Multigene family; Alternative splicing.

FT DOMAIN 1 190

FT TRANSMEM 191 209

FT DOMAIN 210 247

FT TRANSMEM 248 267

FT DOMAIN 268 276

FT TRANSMEM 277 295

FT DOMAIN 296 308

FT TRANSMEM 309 331

FT DOMAIN 332 344

FT TRANSMEM 345 366

FT DOMAIN 367 414

FT TRANSMEM 415 436

FT DOMAIN 437 585

FT CARBOHYD 220 220

FT CARBOHYD 229 229

FT VARSPPLIC 502 511

FT VARSPPLIC 512 585

FT SEQUENCE 585 AA; 65857 MW; DDAEDD32848E2DCF CRC64;

SO QUERY MATCH

Best Local Similarity 100.0%; Score 79; DB 1; Length 585;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAOPNDPSASEH14

DB 370 GAOPNDPSASEH14 383

RESULT 4

CITE_RAT ID CITE_RAT STANDARD: PRT: 638 AA.

AC P22462; P22461; P22463; Q63735;

DT 01-AUG-1991 (Rel. 19, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.2 (KSHIIITA).

GN KCNC2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS KV3.2B AND KV3.2C).

RC TISSUE-BRAIN:

RX MEDLINE-91348257; PubMed-1879548;

RA Luneau C.J., Wiedmann R., Smith J.S., Williams J.B.,

RT "Shaw-like rat brain potassium channel cDNA's with divergent 3' ends.";

RL FEBS Lett. 288:163-167(1991).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM KV3.2B).

RX MEDLINE-92262488; PubMed-1374908;

RA Baker H., Pollock J., Ellisman M., Kentros C., Miera E., Serodio P.,

RT Weiser M., Rudy B., Fruhling D.;

RL "Region-specific expression of a K⁺ channel gene in brain.";

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM KSHIIITA.1).

RC TISSUE-BRAIN:

RX MEDLINE-90311375; PubMed-2367536;

RA McCormack T., de Miera E.C.V.-S., Rudy B.;

RT "Molecular cloning of a member of a third class of Shaker-family K⁺ channel genes in mammals.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:5227-5231(1990).

RN [4]

RP REVISIONS.

RX MEDLINE-91219512; PubMed-2023956;

RA McCormack T., de Miera E.C.V.-S., Rudy B.;

RT "Molecular cloning of a member of a third class of Shaker-family K⁺ channel genes in mammals.";

RL Proc. Natl. Acad. Sci. U.S.A. 88:4060-4060(1991).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM GT10).

RX MEDLINE-92331599; PubMed-1378392;

RA Rettig J., Wunder F., Stocker M., Lichtinghagen R., Mastiaux F.,

RT Beckh S., Kues W., Pedarzani P., Schroeter K.H., Ruppersberg J.P.,

RL "Characterization of a Shaw-related potassium channel family in rat brain.";

RL EMBO J. 11:2473-2486(1992).

CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF KV3.2 ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.

CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.

CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.

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EMBL: M59211; AAA41819.1; -

EMBL: M59313; AAA41820.1; ALT_SEQ.

EMBL: M84203; AAA42143.1; -

EMBL: M34052; AAA42142.1; -

EMBL: X62839; CAA44643.1; -


```

CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-slb.ch/announce/
CC or send an email to license@isb-slb.ch).
CC -----
CC EMBL; M64676; AAA57263.1; -.
CC DR HSSP; O63734; 12TN.
CC DR MIM; 176265; -.
CC DR INTERPRO; IPRO00636; -.
CC DR INTERPRO; IPRO03091; -.
CC DR PFAM; PF00520; Ion_trans; 1.
CC DR PRINTS; PR00169; KCHANNEL.
CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Glycoprotein; Multigene family; Phosphorylation.
CC FT DOMAIN 1 226 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 227 247 SEGMENT S1 (POTENTIAL).
CC FT DOMAIN 248 277 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 278 298 SEGMENT S2 (POTENTIAL).
CC FT DOMAIN 299 312 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 313 333 SEGMENT S3 (POTENTIAL).
CC FT DOMAIN 334 380 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 381 401 SEGMENT S4 (POTENTIAL).
CC FT DOMAIN 402 422 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 423 443 SEGMENT S5 (POTENTIAL).
CC FT DOMAIN 444 451 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 452 472 SEGMENT S6 (POTENTIAL).
CC FT DOMAIN 473 582 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 582 AA; 64527 MW; 8B8E55AACA33A9F CRC64;

Query Match 59.5%; Score 47; DB 1; Length 582;
Best Local Similarity 53.8%; Pred. No. 2.1;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEHT 13
DY ||:|:| :|:|
Ddb 406 GARSPDRGNDHT 418

RESULT 7
CIRG_RAT
ID CIRG_RAT STANDARD; PRT: 625 AA.
AC O63734;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.4 (RAM3).
GN KCNC4.
OS Rattus norvegicus (rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92331599; PubMed=1378392;
RA Bech S., Kues W., Pedarzani P., Schroeter K.H., Ruppersberg J.P.,

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RA  Veh R., Pongs O.:
RT  "Characterization of a Shaw-related potassium channel family in rat
RL  brain.";
RN  EMBO J. 11:2473-2486(1992).
RP  STRUCTURE BY NMR OF 1-30.
RX  MEDLINE=97152495; PubMed=9000078;
RA  Antz C., Geyer M., Fakler B., Scholt M.K., Guy H.R., Frank R.,
RT  Ruppersberg J.P., Kalblitzer H.R.;
RT  "NMR structure of Kunitz inhibitor gates from mammalian voltage-dependent
RT  potassium channels.";
RL  Nature 385:272-275(1997).
CC  -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC  ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC  CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC  MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC  WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC  GRADIENT.
CC  -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC  -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC  CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC  EVERY THIRD POSITION.
CC  -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC  ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC  COMPARTMENTS.
CC  -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC  CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
CC  -----
CC  CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  entities requires a license agreement (See http://www.isb.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: X62841; CAA44645.1; -.
DR  PDB: 1ZTN; 05-JUN-97.
DR  INTERPRO: IPR000636; -.
DR  INTERPRO: IPR003091; -.
DR  Pfam: PF005520; Ion.trans: 1.
DR  PRINTS: PR00169; KCHANNEL.
KW  Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW  Glycoprotein; Multigene family; Phosphorylation; 3D-structure.
SQ  SEQUENCE 625 AA; 68435 MW; C3A86BC88231FB04 CRC64;

OY  1 GAOPDPSASEPT 13
    ||:|:|:|:|
Db  407 GARESDPGRGNDHT 419

Query Match          59.5%; Score 47; DB 1; Length 625;
Best Local Similarity 53.8%; Pred. No. 2.3;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

RESULT
8
CCAB_MOUSE
ID CCAB_MOUSE STANDARD; PRT: 2327 AA.
AC OS5017; 060609;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM
DE CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL
DE 111) (BITI).
GN CACNA1B OR CACNL1A5 OR CCHN1A OR CACHS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/TTISSUE=BRAIN;

```

RA Hong T., Birnbaumer L.;
 RL "Nucleotide sequence polymorphism of mouse alpha 1."
 RN Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A. (ISOFORMS NB1 AND NB2).
 RC TISSUE-NEUROBLASTOMA;
 RX MEDLINE-94139884; PubMed-8307146;
 RA Coppola T., Walzmann R., Boersot M., Heurteaux C., Romey G.,
 Maltel M.-G., Lazdunski M.;
 RT "Molecular cloning of a murine N-type calcium channel alpha 1 subunit.
 RT Evidence for isoforms, brain distribution, and chromosomal
 localization."
 RL FEBS Lett. 338:1-5(1994).
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
 ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
 IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
 CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
 CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B
 BELONGS TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
 BY OMEGA-COMOTOXIN-GVIA (OMEGA-CTX-GVIA) AND BY OMEGA-AGATOXIN-
 IIA (OMEGA-AGA-IIA). THEY ARE HOWEVER INSENSITIVE TO
 DIHYDROPYRIDINES (DHP), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
 CC CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN
 DIRECTED MIGRATION OF IMMATURE NEURONS.
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
 COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
 IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
 FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
 SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
 CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
 LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: NB1 (SHOWN HERE) AND NB2; ARE
 PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION THROUGHOUT THE BRAIN.
 CC HIGHEST LEVELS IN PYRAMIDAL CELL LAYERS C1, C2 AND C3 OF THE
 HIPPOCAMPUS, IN THE DENTATE GYRUS, IN THE CORTEX LAYERS 2 ET 4, IN
 THE SUBICULUM AND THE HABENULA.
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
 POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
 PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -1- PTM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND CGPK
 (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 FAMILY.
 CC -1- CAUTION: REP.2 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 1924
 TO 1934 AND 2121 TO 2127 DUE TO FRAMESHIFTS.
 CC -----
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF042317; AAB97840.1; -
 DR EMBL: U04999; AAB60437.1; ALT_FRAME.
 DR MGD: MG1:88296; CACNALB.
 DR INTERPRO: IPR000636; -
 DR INTERPRO: IPR002077; -
 DR PIR: P00520; Ion.trans. 4.
 DR PRINTS: PRO0167; CACHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation; ATP-binding; Alternative splicing;
 KW Polymorphism.
 FT REPEAT 82 359 I.
 FT REPEAT 468 712 II.
 FT REPEAT 1126 1412 III.

FT REPEAT 1449 1702
 FT DOMAIN 1 95
 FT TRANSMEM 96 114
 FT DOMAIN 115 133
 FT TRANSMEM 134 151
 FT DOMAIN 152 164
 FT TRANSMEM 165 179
 FT DOMAIN 180 186
 FT TRANSMEM 187 205
 FT DOMAIN 206 225
 FT TRANSMEM 226 245
 FT DOMAIN 246 311
 FT TRANSMEM 332 356
 FT DOMAIN 357 482
 FT TRANSMEM 483 502
 FT DOMAIN 503 516
 FT TRANSMEM 517 536
 FT DOMAIN 537 544
 FT TRANSMEM 545 563
 FT DOMAIN 564 574
 FT TRANSMEM 575 592
 FT DOMAIN 593 611
 FT TRANSMEM 612 631
 FT DOMAIN 632 684
 FT TRANSMEM 685 709
 FT DOMAIN 710 1134
 FT TRANSMEM 1135 1158
 FT DOMAIN 1159 1175
 FT TRANSMEM 1176 1195
 FT DOMAIN 1196 1203
 FT TRANSMEM 1204 1226
 FT DOMAIN 1227 1241
 FT TRANSMEM 1242 1256
 FT DOMAIN 1257 1277
 FT TRANSMEM 1278 1297
 FT DOMAIN 1298 1383
 FT TRANSMEM 1384 1408
 FT DOMAIN 1409 1465
 FT TRANSMEM 1466 1484
 FT DOMAIN 1485 1498
 FT TRANSMEM 1499 1518
 FT DOMAIN 1519 1527
 FT TRANSMEM 1528 1546
 FT DOMAIN 1547 1554
 FT TRANSMEM 1555 1573
 FT DOMAIN 1574 1592
 FT TRANSMEM 1593 1612
 FT DOMAIN 1613 1674
 FT TRANSMEM 1675 1694
 FT DOMAIN 1695 2327
 FT TRANSMEM 2040 2044
 FT DOMAIN 2106 2110
 FT TRANSMEM 379 396
 FT ND_BIND 451 458
 FT SITE 314 314
 FT SITE 663 663
 FT SITE 1358 1358
 FT SITE 1646 1646
 FT MOD_RES 1710 1710
 FT CARBOHYD 1728 1739
 FT CARBOHYD 256 256
 FT CARBOHYD 1554 1554
 FT CARBOHYD 1666 1666
 FT VARSPPLIC 756 756
 FT VARIANT 414 414
 FT CONFLICT 238 238
 FT CONFLICT 645 645

IV.
 CYTOPLASMIC (POTENTIAL).
 S1 OF REPEAT I (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S2 OF REPEAT I (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S3 OF REPEAT I (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S4 OF REPEAT I (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S5 OF REPEAT I (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S6 OF REPEAT I (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S1 OF REPEAT II (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S2 OF REPEAT II (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S3 OF REPEAT II (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S4 OF REPEAT II (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S5 OF REPEAT II (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S6 OF REPEAT II (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S1 OF REPEAT III (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S2 OF REPEAT III (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S3 OF REPEAT III (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S4 OF REPEAT III (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S5 OF REPEAT III (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S6 OF REPEAT III (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S1 OF REPEAT IV (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S2 OF REPEAT IV (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S3 OF REPEAT IV (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S4 OF REPEAT IV (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 S5 OF REPEAT IV (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 S6 OF REPEAT IV (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 POLY-HIS.
 POLY-SER.
 BINDING TO THE BETA SUBUNIT (BY
 SIMILARITY).
 ATP (POTENTIAL).
 CALCIUM ION SELECTIVITY AND PERMEABILITY
 (BY SIMILARITY).
 CALCIUM ION SELECTIVITY AND PERMEABILITY
 (BY SIMILARITY).
 CALCIUM ION SELECTIVITY AND PERMEABILITY
 (BY SIMILARITY).
 CALCIUM ION SELECTIVITY AND PERMEABILITY
 (BY SIMILARITY).
 CALCIUM ION SELECTIVITY AND PERMEABILITY
 (BY SIMILARITY).
 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 BY SIMILARITY.
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 A -> AFGKOTGTVSRSSSVSSVNSP (IN ISOFORM
 NB2).
 D -> DA.
 A -> G (IN REF. 2).
 N -> I (IN REF. 2).

FT CONFLICT 757 759 ROO -> OE (IN REF. 2).
 FT CONFLICT 880 880 A -> P (IN REF. 2).
 FT CONFLICT 1128 1128 L -> F (IN REF. 2).
 FT CONFLICT 1173 1173 K -> E (IN REF. 2).
 FT CONFLICT 1185 1185 F -> C (IN REF. 2).
 FT CONFLICT 1227 1230 MISSING (IN REF. 2).
 FT CONFLICT 1388 1388 F -> L (IN REF. 2).
 FT CONFLICT 1549 1549 A -> AET (IN REF. 2).
 FT CONFLICT 1615 1615 I -> S (IN REF. 2).
 FT CONFLICT 1636 1636 L -> I (IN REF. 2).
 FT CONFLICT 1657 1657 G -> D (IN REF. 2).
 FT CONFLICT 1802 1837 MISSING (IN REF. 2).
 FT CONFLICT 1942 1942 A -> G (IN REF. 2).
 FT CONFLICT 1949 1949 G -> D (IN REF. 2).
 FT CONFLICT 1963 1963 A -> K (IN REF. 2).
 FT CONFLICT 1979 1979 A -> L (IN REF. 2).
 FT CONFLICT 1994 1994 E -> D (IN REF. 2).
 FT CONFLICT 2021 2021 H -> D (IN REF. 2).
 FT CONFLICT 2075 2075 A -> AA (IN REF. 2).
 FT CONFLICT 2141 2141 T -> A (IN REF. 2).
 FT CONFLICT 2168 2168 S -> I (IN REF. 2).
 FT CONFLICT 2309 2309 S -> N (IN REF. 2).
 FT CONFLICT 2313 2313 R -> G (IN REF. 2).
 FT CONFLICT 2316 2316 H -> A (IN REF. 2).
 SO SEQUENCE 2327 AA; 261479 MW; AD42CDD38482855A CRC64;

Query Match 55.7%; Score 44; DB 1; Length 2327;
 Best Local Similarity 58.3%; Pred. No. 31;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEH 12
 1:11:111:1
 DB 1057 GSOPDPTVH 1068

RESULT 9
 CCAB-RAT STANDARD; PRG: 2336 AA.
 ID CCAB-RAT

AC 002294;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII).
 GN CACNA1B OR CACNA1A5 OR CACNA5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RA MEDLINE-92279265; PubMed-1317580;
 RA Dubel S.J., Start T.V.B., Hell J., Ahlman M.K., Eysaert J.J., Catterall W.A., Snutch T.P.;
 RT "Molecular cloning of the alpha-1 subunit of an omega-conotoxin-sensitive calcium channel."
 RT Proc. Natl. Acad. Sci. U.S.A. 89:5058-5062(1992).
 RN [2]
 RP SEQUENCE OF 1516-1679 FROM N.A. (CLONE RBB-10).
 RX MEDLINE-90239020; PubMed-1692134;
 RA Snutch T.P., Leonard J.P., Gilbert M.M., Lester H.A., Davidson N.;
 RT "Rat brain expresses a heterogeneous family of calcium channels."
 RT Proc. Natl. Acad. Sci. U.S.A. 87:3391-3395(1990).
 RN [3]
 RP PHOSPHORYLATION.
 RX MEDLINE-94171759; PubMed-8125957;
 RA Hell J.W., Applebury S.M., Yokoyama C.T., Warner C., Catterall W.A.;
 RT "Differential phosphorylation of two size forms of the N-type calcium channel alpha 1 subunit which have different COOH termini."
 RT J. Biol. Chem. 269:7390-7396(1994).

RN [4]
 RP BETA-SUBUNIT BINDING DOMAIN
 RX MEDLINE-94150724; PubMed-7509046;
 RA Pragnell M., de Waard M., Mori Y., Tanabe T., Snutch T.P., Campbell K.P.;
 RT "Calcium channel beta-subunit binds to a conserved motif in the I-II cytoplasmic linker of the alpha-1 subunit."
 RT Nature 368:67-70(1994)
 CC -I- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY OMEGA-CONOTOXIN-GVIA (OMEGA-CGX-GVIA) AND BY OMEGA-AGATOXIN-IIIa (OMEGA-AGA-IIIa). THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN DIRECTED MIGRATION OF IMMATURE NEURONS.
 CC -I- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -I- ALTERNATIVE PRODUCTS: THERE SEEMS TO BE TWO ISOFORMS THAT DIFFER IN THEIR C-TERMINAL REGION; THEY ARE PROBABLY PRODUCED BY ALTERNATIVE SPLICING.
 CC -I- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM.
 CC -I- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -I- PTM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND GSKP.
 CC -I- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.
 CC -----
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 CC -----
 DR EMBL; M92905; AAA42014.1; -
 DR INTERPRO; IPR000636; -
 DR INTERPRO; IPR002077; -
 DR PFAM; PF00520; ion_trans; 4.
 DR PRINTS; PR00167; CACNANL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation; ATP-binding; Alternative splicing.
 FT REPEAT 82 359 II.
 FT REPEAT 469 713 I.
 FT REPEAT 1135 1421 IIT.
 FT REPEAT 1458 1711 IV.
 FT DOMAIN 1 95 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 96 114 S1 OF REPEAT I (POTENTIAL).
 FT DOMAIN 115 133 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 134 151 S2 OF REPEAT I (POTENTIAL).
 FT DOMAIN 152 164 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 165 179 S3 OF REPEAT I (POTENTIAL).
 FT DOMAIN 180 186 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 187 205 S4 OF REPEAT I (POTENTIAL).
 FT DOMAIN 206 225 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 226 245 S5 OF REPEAT I (POTENTIAL).
 FT DOMAIN 246 331 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 332 356 S6 OF REPEAT I (POTENTIAL).

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FT DOMAIN 357 483 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 484 503 S1 OF REPEAT II (POTENTIAL).
FT DOMAIN 504 517 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 518 537 S2 OF REPEAT II (POTENTIAL).
FT DOMAIN 538 545 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 546 564 S3 OF REPEAT II (POTENTIAL).
FT DOMAIN 565 575 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 576 593 S4 OF REPEAT II (POTENTIAL).
FT DOMAIN 594 612 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 613 632 S5 OF REPEAT II (POTENTIAL).
FT DOMAIN 633 685 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 686 710 S6 OF REPEAT II (POTENTIAL).
FT DOMAIN 711 1143 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1144 1167 S1 OF REPEAT III (POTENTIAL).
FT DOMAIN 1168 1184 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1185 1204 S2 OF REPEAT III (POTENTIAL).
FT DOMAIN 1205 1212 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1213 1235 S3 OF REPEAT III (POTENTIAL).
FT DOMAIN 1236 1250 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1251 1265 S4 OF REPEAT III (POTENTIAL).
FT DOMAIN 1266 1286 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1287 1306 S5 OF REPEAT III (POTENTIAL).
FT DOMAIN 1307 1392 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1393 1417 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1418 1474 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1475 1493 S1 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1494 1507 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1508 1527 S2 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1528 1536 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1537 1555 S3 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1556 1563 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1564 1582 S4 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1583 1601 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1602 1621 S5 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1622 1683 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1684 1703 S6 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1704 2336 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 2049 2053 POLY-SER.
FT DOMAIN 2115 2119 BINDING TO THE BETA SUBUNIT.
FT TRANSSEM 379 396 ATP (POTENTIAL).
FT DOMAIN 452 459 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT TRANSSEM 314 314 (BY SIMILARITY).
FT SITE 664 664 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT TRANSSEM 1367 1367 (BY SIMILARITY).
FT SITE 1655 1655 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT TRANSSEM 1719 1719 (BY SIMILARITY).
FT MOD_RES 1737 1748 PHOSPHORYLATION (BY CARP) (POTENTIAL).
FT CA_BIND 256 256 BY SIMILARITY.
FT CARBOHYD 1563 1563 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1675 1675 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1538 1538 N -> D (IN REF. 2).
FT CONFLICT 1579 1579 C -> L (IN REF. 2).
SQ SEQUENCE 2336 AA; 262254 MW; 8D50AF67834FD1BC CRC64;

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Query Match 55.7%; Score 44; DB 1; Length 2336;
 Best Local Similarity 58.3%; Pred. No. 31;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 GAQPNPDSASEH 12
 Db 1066 GSQSPDSSTVH 1077

RESULT 10
 Y194 HUMAN
 ID 012766;
 AC 01-NOV-1997 (Rel. 35, Created)
 STANDARD; PRT; 1435 AA.

```

DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL PROTEIN KIA0194 (FRAGMENT).
GN KIA0194
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW.
RX MEDLINE=96281124; PubMed=8724849;
RA Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. V.
RT The coding sequences of 40 new genes (KIA0161-KIA0200) deduced by
RT analysis of cDNA clones from human cell line KG-1."
RL DNA Res. 3:17-24(1996).
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CC -----
DR EMBL; D83778; BAA12107.1; -.
DR INTERPRO; IPR000910; -.
DR PFM; PFM0505; HMG-box; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 1435 AA; 156908 MW; 404692C02E81F07A CRC64;

```

Query Match 53.2%; Score 42; DB 1; Length 1435;
 Best Local Similarity 60.0%; Pred. No. 38;
 Matches 9; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

OY 1 GAQPN-DPSASEH 13
 Db 1319 GLQPNPGDSAGHS 1333

RESULT 11
 DVL3_HUMAN
 ID DVL3_HUMAN STANDARD; PRT; 716 AA.
 AC 092997; 092607; 014642; 013531;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE SEGMENT POLARITY PROTEIN DISHEVELLED HOMOLOG DVL-3 (DISHEVELLED-3)
 DE (DSH HOMOLOG 3) (KIA0208).
 GN DVL3.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=96008870; PubMed=9344861;
 RA Bui T.D., Beier D.R., Jonssen M., Smith K., Dorrington S.M.,
 RA Kellman L., Kearney L., Regan R., Sussman D.J., Harris A.L.;
 RT "cDNA cloning of a human dishevelled DVL-3 gene, mapping to 3q27, and
 RT expression in human breast and colon carcinomas."
 RL Biochem. Biophys. Res. Commun. 239:510-516(1997).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97336056; PubMed=9192851;
 RA Semenov M.V., Snyder M.;
 RT "Human dishevelled genes constitute a DHR-containing multigene
 RT family."
 RL Genomics 42:302-310(1997).
 RL [3]
 RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;
RX MEDLINE-96414301: PubMed-8817329;
RA Pizzuti A., Amati F., Calabrese G., Mari A., Colosimo A., Silani V.,
RA Giardinò L., Ratti A., Penso D., Calza L., Palka G., Scariato G.,
RA Novelli G., Dallapiccola B.;
RT "cDNA characterization and chromosomal mapping of two human homologues
RT of the Prosoplia dishevelled polarity gene.";
RL Hum. Mol. Genet. 5:953-958(1996).
[4]
RN SEQUENCE FROM N.A.
RP TISSUE-BONE MARROW;
RX MEDLINE-97191544; PubMed-9039502;
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (K1AA0201-K1AA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain.";
RL DNA Res. 3:321-329(1996).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY
CC
CC -1- MEDIATED BY MULTIPLE WNT GENES.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 PDZ/DRH DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE DSH FAMILY.
CC -----
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CC -----
DR EMBL: U75651; AAB84228.1; -;
DR EMBL: AF006013; AAB65244.1; -;
DR EMBL: U49262; AAB47447.1; -;
DR EMBL: D86963; BAA1319.1; -;
DR HSSP: P31016; 1BFE.
DR MIM: 601368; -;
DR INTERPRO: IPR000591; -;
DR INTERPRO: IPR001158; -;
DR INTERPRO: IPR001478; -;
DR PFWAM: PF00610; DEP: 1.
DR PFWAM: PF00778; DIX: 1.
DR PFWAM: PF00595; PDZ: 1.
KW Developmental protein.
KW DOMAIN 249 336
FT FT CONFLICT 2 2 DHR.
FT CONFLICT 76 76 G-> D (IN REF. 3).
FT CONFLICT 102 102 S-> Y (IN REF. 1).
FT CONFLICT 151 151 P-> S (IN REF. 3).
FT CONFLICT 182 182 G-> W (IN REF. 3).
FT CONFLICT 218 218 S-> R (IN REF. 3).
FT CONFLICT 222 222 K-> N (IN REF. 3).
FT CONFLICT 222 222 R-> W (IN REF. 3).
FT CONFLICT 230 230 E-> D (IN REF. 3).
FT CONFLICT 233 233 S-> C (IN REF. 3).
FT CONFLICT 236 236 S-> T (IN REF. 3).
FT CONFLICT 239 239 T-> S (IN REF. 3).
FT CONFLICT 242 242 T-> A (IN REF. 3).
FT CONFLICT 303 303 N-> K (IN REF. 3).
FT CONFLICT 431 431 R-> C (IN REF. 3).
FT CONFLICT 450 450 W-> C (IN REF. 3).
FT CONFLICT 465 465 R-> P (IN REF. 3).
FT CONFLICT 472 472 L-> V (IN REF. 3).
FT CONFLICT 543 543 P-> R (IN REF. 2).
FT CONFLICT 554 554 FP-> LG (IN REF. 2).
FT CONFLICT 629 629 A-> T (IN REF. 3).
FT CONFLICT 633 633 S-> I (IN REF. 3).
FT CONFLICT 682 716 PPGRLASVPELTSKQSPFMANGNSEFFVDVW -> LR
SQ SEQUENCE 716 AA; 78054 MM; BIA55EBF9507D08E CRC64;
Query Match 49.4%; Score 39; DB 1; Length 716;

Best Local Similarity 46.2%; Pred. No. 56;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 2 AQPNDPSASERTH 14
Db 622 SERSGPASERSH 634
:::|||||:
DYL3_MOUSE STANDARD; PRT; 716 AA.
AC 061062;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SEGMENT POLARITY PROTEIN DISHEVELLED HOMOLOG DVL-3 (DISHEVELLED-3)
DE (DSH HOMOLOG 3).
GN DVL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE-97081279; PubMed-8922524;
RA Tseng M., Liyam N., Yang Y., Belier D.R., Wynshaw-Boris A.,
RA Susman D.J.;
RT "Isolation and characterization of mouse dishevelled-3.";
RL Dev. Dyn. 207:253-262(1996).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY
CC
CC -1- MEDIATED BY MULTIPLE WNT GENES.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: UBQUITOUS.
CC -1- SIMILARITY: CONTAINS 1 PDZ/DRH DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE DSH FAMILY.
CC -----
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CC -----
DR EMBL: U41285; AAB01761.1; -;
DR HSSP: P31016; 1BFE.
DR MGD: MGI:108100; DVL3.
DR INTERPRO: IPR000591; -;
DR INTERPRO: IPR001158; -;
DR INTERPRO: IPR001478; -;
DR PFWAM: PF00610; DEP: 1.
DR PFWAM: PF00778; DIX: 1.
DR PFWAM: PF00595; PDZ: 1.
KW Developmental protein.
KW DOMAIN 249 336 DHR.
SQ SEQUENCE 716 AA; 78122 MM; 35412C03202301P0 CRC64;
Query Match 49.4%; Score 39; DB 1; Length 716;
Best Local Similarity 46.2%; Pred. No. 56;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 2 AQPNDPSASERTH 14
Db 622 SERSGPASERSH 634
:::|||||:
DYL3_MOUSE STANDARD; PRT; 1060 AA.
AC P49413;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)


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FT CONFLICT 496 496 K -> R (IN REF. 4).
FT CONFLICT 519 519 G -> GG (IN REF. 4).
FT CONFLICT 551 572 LNVSVLGVSRCGTTISTESTF -> IECDHMYKEPLEEQ
FT CONFLICT 594 594 RLVDNYV (IN REF. 4).
FT CONFLICT 687 690 F -> N (IN REF. 4).
FT CONFLICT 721 721 ELYP -> GIIS (IN REF. 4).
FT CONFLICT 823 832 A -> R (IN REF. 4).
FT CONFLICT 836 837 SNRCETSAVP -> LNVSVRCA (IN REF. 4).
FT CONFLICT 902 902 GN -> WD (IN REF. 4).
FT CONFLICT 1015 1015 E -> R (IN REF. 4).
FT CONFLICT 1015 1015 G -> V (IN REF. 4).
SQ SEQUENCE 1136 AA; 127764 MW; 8AC4E8C26FE3E9B5 CRC64;
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Query Match 49.4%; Score 39; DB 1; Length 1136;
Best Local Similarity 45.5%; Pred. No. 93;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHTH 14
|||:||||
DB 433 PNOPTVNDTH 443

```
RESULT 15
RBP1_PLAVB
ID RBP1_PLAVB STANDARD: PRT: 2869 AA.
AC 000798.
DC 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE RETICULOCYTE BINDING PROTEIN 1 PRECURSOR.
GN RBP1.
OS Plasmodium vivax (strain Belen).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92315338; PubMed=1617731;
RA Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.;
RT "A reticulocyte-binding protein complex of Plasmodium vivax
merozoites."
RL Cell 69:1213-1226(1992).
CC -!- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO
HUMAN RETICULOCYTE CELLS.
CC -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
CC -----
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CC -----
DR EMBL: M88097; AAA29743.1; -.
DR HSSP: P36956; IAM9.
KW Malaria; Receptor; Signal; Transmembrane.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 2869 RETICULOCYTE BINDING PROTEIN 1.
FT DOMAIN 18 2807 EXTRACELLULAR.
FT TRANSMEM 2808 2826 POTENTIAL.
FT DOMAIN 2827 2869 CYTOPLASMIC.
FT SITE 1030 1032 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 1030 1032 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 2599 2601
SQ SEQUENCE 2869 AA; 330213 MW; B9DBE44205EBCF CRC64;
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DB 2695 NDPQSEHTH 2704

Search completed: February 2, 2001, 10:41:50
Job time: 314 sec

Query Match 49.4%; Score 39; DB 1; Length 2869;
Best Local Similarity 70.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 NDPASASEHTH 14
|||:||||

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OM protein - protein search, using sw model

Run on: February 2, 2001, 10:39:09 ; Search time 62.83 Seconds
(without alignments)
26.117 Million cell updates/sec

Title: US-09-273-217-3
Perfect score: 79
Sequence: 1 GAQPNPDSASEH14

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.15:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	585	6 Q9XSJ8	Q9XSJ8 canis faml
2	70	88.6	587	13 Q9IA29	Q9IA29 oncorhynch
3	59	74.7	279	13 Q9IA28	Q9IA28 oncorhynch
4	52	65.8	273	2 Q9ZBS9	Q9ZBS9 streptomyc
5	47	59.5	325	10 Q65152	Q65152 malus domes
6	45	57.0	180	5 Q9VW73	Q9VW73 drosophila
7	45	57.0	214	2 Q9RYV3	Q9RYV3 deinococcus
8	44	55.7	872	5 Q9VAMS	Q9VAMS drosophila
9	44	55.7	2333	11 Q89089	Q89089 rattus norv
10	42	53.2	378	4 Q9UMF4	Q9UMF4 homo sapien
11	42	53.2	592	13 Q9PVD1	Q9PVD1 xenopus lae
12	42	53.2	803	3 Q13657	Q13657 schizosacch
13	42	53.2	1932	3 Q06409	Q06409 saccharomyc
14	41	51.9	209	3 Q9P7C6	Q9P7C6 schizosacch
15	41	51.9	276	2 Q9X908	Q9X908 streptomyc
16	41	51.9	276	2 Q9X9S4	Q9X9S4 streptomyc
17	41	51.9	325	10 Q9ZVMS	Q9ZVMS arabidopsis
18	41	51.9	435	10 Q9XEU9	Q9XEU9 oryza sativ
19	40	50.6	615	11 Q9J398	Q9J398 mus musculu

20	40	50.6	757	6 Q9N015	Q9N015 macaca fasc
21	40	50.6	1711	5 Q96108	Q96108 plasmodium
22	40	50.6	6420	2 P95814	P95814 streptomyc
23	39	49.4	327	10 Q04391	Q04391 eucalyptus
24	39	49.4	339	2 Q56136	Q56136 salmoneilla
25	39	49.4	343	2 Q56026	Q56026 salmoneilla
26	39	49.4	348	2 Q56033	Q56033 salmoneilla
27	39	49.4	354	6 Q9M230	Q9M230 oryctolagus
28	39	49.4	457	4 Q13518	Q13518 homo sapien
29	39	49.4	508	12 Q65579	Q65579 bovine herp
30	39	49.4	548	4 Q9UG07	Q9UG07 homo sapien
31	39	49.4	603	2 Q46547	Q46547 bacteroides
32	39	49.4	683	5 Q09977	Q09977 caenorhabdi
33	39	49.4	701	5 Q24928	Q24928 elmeria ten
34	39	49.4	2656	5 Q9NE92	Q9NE92 leishmania
35	38	48.1	63	5 Q9VHW2	Q9VHW2 drosophila
36	38	48.1	114	12 Q86574	Q86574 human herpe
37	38	48.1	118	10 Q9XH41	Q9XH41 nicotiana t
38	38	48.1	177	10 P93003	P93003 arabidopsis
39	38	48.1	208	2 P95581	P95581 pseudomonas
40	38	48.1	222	2 P74298	P74298 synechocyst
41	38	48.1	286	3 Q9P5D1	Q9P5D1 neurospora
42	38	48.1	296	2 Q9RY19	Q9RY19 deinococcus
43	38	48.1	338	5 Q9VIR3	Q9VIR3 drosophila
44	38	48.1	350	5 Q21249	Q21249 caenorhabdi
45	38	48.1	373	13 Q92073	Q92073 g beta-1,4-

ALIGNMENTS

RESULT 1
ID Q9XSJ8 PRELIMINARY: PRT: 585 AA.
AC Q9XSJ8;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-UN-2000 (TREMBLrel. 14, Last annotation update)
GN KV3.1.
DE KV3.1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ATRIUM;
RA Yue L., Mang'Z., Rindt H., Nattel S.;
RT "Cloning and functional expression of cardiac Kv3.1 channels: A novel
RT molecular basis for cardiac delayed rectifier currents."
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF153198; AAD34618.1; -
DR INTERPRO: IPR000636; -
DR INTERPRO: IPR001622; -
DR INTERPRO: IPR003091; -
DR PFM: PF00520; ion_trans; 1.
DR PRINTS: PR00169; KCHANNEL.
SQ SEQUENCE 585 AA; 65911 MW; 71A0805FAE64AAAE CRC64;

Query Match 100.0%; Score 79; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 1,7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAQPNPDSASEH14
DB 370 GAQPNPDSASEH14 383

RESULT 2
Q9IA29
ID Q9IA29; PRELIMINARY: PRT: 587 AA.

DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE SHAW-RELATED POTASSIUM CHANNEL PROTEIN RAW1.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Panofen F., Rahe H., Stegmann J., Jeserich G.;
 RT "Molecular cloning and functional characterization of Shaw-related
 RL potassium channels of trout CNS."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF223409; AAF33249.1; -
 KW Ionic channel.
 SQ SEQUENCE 587 AA; 66317 MW; A0CB46FA3CF17E86 CRC64;

Query Match 88.6%; Score 70; DB 13; Length 587;
 Best Local Similarity 85.7%; Pred. No. 0.00057;
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEH14
 ||:|||||
 DB 357 GAKNDPRASEH14 370

RESULT 3
 OY1A28 PRELIMINARY; PRT; 279 AA.

AC 091A28;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE SHAW-RELATED POTASSIUM CHANNEL PROTEIN RAW2 (FRAGMENT).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Panofen F., Rahe H., Stegmann J., Jeserich G.;
 RT "Molecular cloning and functional characterization of Shaw-related
 RL potassium channels of trout CNS."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF223410; AAF33250.1; -
 KW Ionic channel.
 FT NON_TER 1
 FT NON_TER 279
 SQ SEQUENCE 279 AA; 31585 MW; 34837398B528B65 CRC64;

Query Match 74.7%; Score 59; DB 13; Length 279;
 Best Local Similarity 76.9%; Pred. No. 0.02;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEH13
 ||:|||||
 DB 253 GAKNDPRASEH13 265

RESULT 4
 OY2BS9 PRELIMINARY; PRT; 273 AA.

AC 092BS9;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DE PUTATIVE GNTF FAMILY TRANSCRIPTIONAL REGULATOR.
 GN SCIA9.23.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycesaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Saunders D.C., Harris D.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kleiser H.M., Denapate D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RL the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 DR M01. Microbiol. 21:77-96(1996).
 DR EMBL; AL034446; CAA22393.1; -
 DR INTERPRO; IPR000524; -
 DR PFAM; PF00392; gntR; 1.
 SQ SEQUENCE 273 AA; 28699 MW; B82D49CD374B6F00 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 273;
 Best Local Similarity 57.1%; Pred. No. 0.3;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEH14
 ||:|||||
 DB 43 GAEPDGPARGH14 56

RESULT 5
 OY1A28 PRELIMINARY; PRT; 325 AA.

AC 065152;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE PUTATIVE CINNAMYL ALCOHOL DEHYDROGENASE.
 GN CAD.
 OS Malus domestica (Apple) (Malus sylvestris).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Rosales; Rosaceae; Malus.
 OX NCBI_TaxID=3750;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. FUJI;
 RA Lee J.-R., An G., Kim S.-R.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF053084; AAC06319.1; -
 DR MENDEL; 28908; Maldo; 2995; 28908.
 SQ SEQUENCE 325 AA; 35553 MW; 1AB7F5117ADA60CE CRC64;

Query Match 59.5%; Score 47; DB 10; Length 325;
 Best Local Similarity 63.6%; Pred. No. 2.5;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPASEH14
 ||||:||||
 DB 40 PNDPTEH14 50


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RESULT 6
Q9VW73 PRELIMINARY; PRT; 180 AA.
ID Q9VW73
AC Q9VW73
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG14184 PROTEIN.
GN CG14184.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brotlier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iodgwan C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mottel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
RA Palazono M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spletter E., Spredling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003515; AAF49076.1;
DR FLVBAS; FB900036932; CG14184.
SQ SEQUENCE 180 AA; 20507 MW; 6BD11AA8107EECF4 CRC64;

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AC Q9RYX3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE HYPOTHEITICAL 22.6 KDA PROTEIN.
GN DRA0170.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.S., Lam P., McDonald L., Utecherback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome Sequence of the Radioresistant Bacterium Deinococcus
RT radiodurans R1."
RL Science 286:1571-1577(1999).
DR EMBL; AE001862; AAF12308.1;
DR TIGR; DRA0170;
KW Hypothetical protein.
SQ SEQUENCE 214 AA; 22623 MW; 387D762D007D8F35 CRC64;

Query Match 57.0%; Score 45; DB 2; Length 214;
Best Local Similarity 66.7%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAOPNDPSESEH 12
DB 129 GAOPNDPSESEH 140

RESULT 8
Q9VAM5 PRELIMINARY; PRT; 872 AA.
ID Q9VAM5
AC Q9VAM5
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CG14514 PROTEIN.
GN CG14514.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brotlier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

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Query Match	55.7%	Score 44:	DB 5;	Length 872;
Best Local Similarity	70.0%;	Pred. No. 21;		
Matches	7;	Conservative	2;	Mismatches
			1;	Indels
				Gaps
Oy	4	PNPSPASERT	13	
	11	1::1111		
Db	713	PNPSPASERT	722	

TV sustaineri upregulirani

RT Potassium Channel Gene Encoding a Delayed Rectifier Current.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF132853; AAD52813.1; -.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR001622; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFM: PF00520; Ion_trans; 1.
DR PFM: PF02214; K_tetra; 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel.
SQ SEQUENCE 592 AA; 66891 MW; 882FAA230BDD8E8 CRC64;

Query Match 53.2%; Score 42; DB 13; Length 592;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAOPNDPSASERTH 14
|||:|:|:|:
DB 351 GADPDITGSKHTY 364

RESULT 12
ID 013657 PRELIMINARY; PRT: 803 AA.
AC 013657;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PROBABLE MEMBRANE PROTEIN YOL130W.
GN P1066 OR SPBC27B12.12C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Schizosaccharomycetaceae; Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972 H-;
RA Kushiida N., Yamazaki S., Tanaka T., Jinno K., Haikawa Y., Yamazaki J.,
RA Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai M., Aoki K.,
RA Ogura K., Otsuka R., Kodoh Y., Yanagida M., Machida M., Zhang M.Q.,
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Wood V., Rajandream M.A., Barrell B.G., Lauber J., Hilbert H.,
RA Duesterhoeft A.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB004538; BAA21447.1; -.
DR EMBL; AL021766; CAA16907.1; -.
DR EMBL; AB004539; BAA21448.1; -.
DR INTERPRO: IPR002523; -.
DR PFM: PF01544; CORA; 1.
KW Hypothetical protein.
SQ SEQUENCE 803 AA; 89396 MW; 5E1DB270D9D83572 CRC64;

Query Match 53.2%; Score 42; DB 3; Length 803;
Best Local Similarity 63.6%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 PNDPSASERTH 14
||||:|:|:
DB 418 PNDPSSLSHSN 428

RESULT 13
ID 006409 PRELIMINARY; PRT: 1932 AA.
AC 006409;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE CHROMOSOME XII COSMID 9576.
GN L9576.7.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RX MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansgore W.,
RA Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,
RA Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K.,
RA Heuss-Neltzel D., Hilbert H., Hilger F., Kiehn K., Kotter P.,
RA Louis E.J., Messenguy F., Mewes H.W., Mosga T., Mostl D.,
RA Muller-Auer S., Nentwich U., Obermaier B., Pivavadi E., Pohl T.M.,
RA Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
RA Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,
RA Underwood A.P., Uristarazu L.A., Vandenbol M., Verhasselt P.,
RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hohnselt J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Favella A.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Waterston R.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Cherry J.M.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U20939; AAB67508.1; -.
SQ SEQUENCE 1932 AA; 221561 MW; 1E9CE4AE6F8D3F94 CRC64;

Query Match 53.2%; Score 42; DB 3; Length 1932;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 GAOPNDPSASERTH 14
||||:|:|:
DB 1913 GSOPNTNDSQHKH 1926

RESULT 14
ID 09P7C6 PRELIMINARY; PRT: 209 AA.
AC 09P7C6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE DNA PROTEIN (FRAGMENT).
GN SPC10H11.02.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Schizosaccharomycetaceae; Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Saunders D., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL162771; CAB85447.1; -.
FT NON TER 209
SQ SEQUENCE 209 AA; 25323 MW; 020E519442A56AA2 CRC64;

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OM protein - protein search, using sw model

Run on: February 2, 2001, 10:37:11 ; Search time 38.22 Seconds

(without alignments)
24.872 Million cell updates/sec

Title: US-09-273-217-3

Sequence: 1 GAOPNDPSASEH14

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 6790655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR66:*

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	79	100.0	511	2 A46020	potassium channel
2	79	100.0	511	2 S07095	potassium channel
3	79	100.0	585	2 A39395	delayed rectifier
4	71	89.9	581	2 S17150	potassium channel
5	71	89.9	613	2 A39402	potassium channel
6	71	89.9	624	2 S22703	voltage-gated pota
7	52	65.8	273	2 T34672	probable gntx faml
8	47	59.5	325	2 T16995	probable cinnamyl-
9	47	59.5	625	2 S13919	potassium channel
10	45	57.0	214	2 E75613	hypothetical prote
11	44	55.7	2288	2 S41080	calcium channel al
12	44	55.7	2336	2 A45386	omega-conotoxin-se
13	42	53.2	803	2 T40036	hypothetical prote
14	42	53.2	1932	2 S53409	probable membrane
15	41	51.9	276	2 T45275	oxidoreductase of
16	40	50.6	1711	2 C71625	variant-specific s
17	40	50.6	6420	2 T30283	polypeptide synthas
18	39	49.4	327	2 T10736	cinnamyl-alcohol d
19	39	49.4	339	2 S70218	slip protein - Sal
20	39	49.4	343	2 S70549	glycoprotein gc -
21	39	49.4	508	2 S54264	hypothetical prote
22	39	49.4	548	2 T14793	hypothetical prote
23	39	49.4	683	2 T34103	discovered protei
24	39	49.4	716	2 J05763	putative utilization
25	39	49.4	1060	2 S54779	parasporeal crystal
26	39	49.4	1136	1 USBS81	reticulocyte-bind
27	39	49.4	2829	1 A42771	basic transactivat
28	38	48.1	114	2 T40511	Terminal flower1
29	38	48.1	177	2 T48411	

30	38	48.1	222	2 S76133	sensory transducti
31	38	48.1	286	2 T49505	hypothetical prote
32	38	48.1	296	2 B75555	probable lipase/es
33	38	48.1	350	2 T16576	hypothetical prote
34	38	48.1	361	2 S19552	potassium channel
35	38	48.1	386	2 T05691	multisubunit chn
36	38	48.1	402	2 T51606	probable 265 prote
37	38	48.1	405	2 T12317	265 proteasome reg
38	38	48.1	452	2 T40769	hypothetical prote
39	38	48.1	474	2 H82564	3-isopropylmalate
40	38	48.1	513	2 S52571	phosphoprotein pho
41	38	48.1	603	2 S27055	basic serine prote
42	38	48.1	679	2 A42073	potassium channel
43	38	48.1	767	2 S5618	hypothetical prote
44	38	48.1	769	2 S5618	Shaw type potassi
45	38	48.1	798	2 S20881	homeotic protein p

ALIGNMENTS

```

RESULT 1
A46020
potassium channel KCNC1 - human
N:Alternate names: potassium channel NGK2-KV4; Shaw-related potassium channel KV3.1
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 19-May-1994 #text_change 05-Nov-1999
C:Accession: A46020; A45072
R:Ried, T.; Rudy, B.; Vega-Saenz de Miera, E.; Lau, D.; Ward, D.C.; Sen, K.
Genomics 15, Rudy, B.; Vega-Saenz de Miera, E.; Lau, D.; Ward, D.C.; Sen, K.
A:Title: Localization of a highly conserved human potassium channel gene (NGK2-KV4; K
A:Reference number: A46020; MUID:93194190
A:Accession: A46020
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-511 <RIB>
A:Cross-references: GB:S56770; NID:9298602; PIDN:AA525764.1; PID:9298603
A:Note: sequence extracted from NCBI backbone (NCBIN:127271, NCBIPI:127272)
R:Grissmer, S.; Ghanashan, S.; Dethlefs, B.; McPherson, J.D.; Wasmuth, J.J.; Guttman,
J. Biol. Chem. 267, 20971-20979, 1992
A:Title: The Shaw-related potassium channel gene, Kv3.1, on human chromosome 11, enco
A:Reference number: A45072; MUID:93016011
A:Accession: A45072
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 244-475 <GRI>
A:Cross-references: GB:M96747; NID:9186672; PIDN:AAA59458.1; PID:9186673
A:Experimental source: Louckes lymphoma cells
A:Note: sequence extracted from NCBI backbone (NCBIP:116151)
C:Genetics:
A:Gene: GDB:KCNC1
A:Cross-references: GDB:128082; OMIM:176258
A:Map position: 11p15.1-11p15.1
C:Keywords: alternative splicing; glycoprotein; potassium channel; transmembrane prot

Query Match 100.0%; Score 79; DB 2; Length 511;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAOPNDPSASEH14
Db 370 GAOPNDPSASEH14 383

RESULT 2
S07095
potassium channel protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
C:Accession: S07095
R:Yokoyama, S.; Imoto, K.; Kawamura, T.; Higashida, H.; Iwabe, N.; Miyata, T.; Numa,
FEBS Lett. 259, 37-42, 1989

```

A:Title: Potassium channels from NG108-15 neuroblastoma-glioma hybrid cells. Primary str
A:Reference number: 507095; MUID:90092535
A:Accession: 507095
A:Molecule type: mRNA
A:Residues: 1-511 <YOK>
A:Cross-references: EMBL:Y07521; NID:g533997; PIDN:CAA68814.1; PID:g533998
C:Keywords: alternative splicing; membrane protein

Query Match 100.0%; Score 79; DB 2; Length 511;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAOPNDPSASEHTH 14
|||||
Db 370 GAOPNDPSASEHTH 383

RESULT 3
A39395
delayed rectifier potassium channel KV4, neuronal - rat
N:Alternate names: potassium channel protein Raw2
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Feb-1992 #sequence, revision 28-Feb-1992 #text, change 05-Nov-1999
C:Accession: A39395; S22704; S19100
R:Lunesu, C.J.; Williams, J.B.; Marshall, J.; Levitan, E.S.; Oliva, C.; Smith, J.S.; Ant
Proc. Natl. Acad. Sci. U.S.A. 88, 3932-3936, 1991
A:Title: Alternative splicing contributes to K(+) channel diversity in the mammalian cer
A:Reference number: A39395; MUID:91219486
A:Accession: A39395
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-585 <LUN>
A:Cross-references: GB:M68880; GB:M37845; NID:g205106; PIDN:AAA41501.1; PID:g205107
R:Retlig, J.; Munder, F.; Stocker, M.; Lichtinghagen, R.; Mastiaux, F.; Beckh, S.; Kues,
EMBO J. 11, 2473-2486, 1992
A:Title: Characterization of a shw-related potassium channel family in rat brain.
A:Reference number: S22702; MUID:92331599
A:Accession: S22704
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-585 <RET>
A:Cross-references: EMBL:X62840; NID:g57652; PIDN:CAA44644.1; PID:g57653
C:Keywords: alternative splicing; glycoprotein; ion channel; leucine zipper; transmembr
F:11-109/Domain: transmembrane #status predicted <TM1>
F:245-266/Domain: transmembrane #status predicted <TM2>
F:278-298/Domain: transmembrane #status predicted <TM3>
F:310-328/Domain: transmembrane #status predicted <TM4>
F:345-364/Domain: transmembrane #status predicted <TM5>
F:415-436/Domain: transmembrane #status predicted <TM6>

Query Match 100.0%; Score 79; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAOPNDPSASEHTH 14
|||||
Db 370 GAOPNDPSASEHTH 383

RESULT 4
S17150
potassium channel protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Nov-1993 #sequence, revision 10-Nov-1995 #text, change 10-Nov-1995
C:Accession: S17150
R:Lunesu, C.; Wiedmann, R.; Smith, J.S.; Williams, J.B.
FEBS Lett. 288, 163-167, 1991
A:Title: Shaw-like rat brain potassium channel cDNA's with divergent 3' ends.
A:Reference number: S17150; MUID:91348257
A:Accession: S17150
A:Molecule type: DNA

A:Residues: 1-581 <LUN>

Query Match 89.9%; Score 71; DB 2; Length 581;
Best Local Similarity 100.0%; Pred. No. 0.000219;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAOPNDPSASEHT 13
|||||
Db 407 GAOPNDPSASEHT 419

RESULT 5
A39402
potassium channel protein IIIA form 1, shaker-type - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Feb-1992 #sequence, revision 28-Feb-1992 #text, change 08-Oct-1999
C:Accession: A39402
R:McCormack, T.; Vega-Saenz de Miera, E.C.; Rudy, B.
Proc. Natl. Acad. Sci. U.S.A. 88, 4060, 1991
A:Reference number: A39402; MUID:91219512
A:Contents: erratum
A:Accession: A39402
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-613 <MCC>
A:Cross-references: GB:M34052; NID:g206913; PIDN:AAA42142.1; PID:g206914

Query Match 89.9%; Score 71; DB 2; Length 613;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAOPNDPSASEHT 13
|||||
Db 407 GAOPNDPSASEHT 419

RESULT 6
S22703
voltage-gated potassium channel protein Raw1 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence, revision 30-Sep-1993 #text, change 05-Nov-1999
C:Accession: S22703; A45292; S19099
R:Retlig, J.; Munder, F.; Stocker, M.; Lichtinghagen, R.; Mastiaux, F.; Beckh, S.; Ku
EMBO J. 11, 2473-2486, 1992
A:Title: Characterization of a shw-related potassium channel family in rat brain.
A:Reference number: S22702; MUID:92331599
A:Accession: S22703
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-624 <RET>
A:Cross-references: EMBL:X62839; NID:g57650; PIDN:CAA44643.1; PID:g57651
R:Rudy, B.; Kentros, C.; Weisner, M.; Fritzliling, D.; Serodio, P.; Vega-Saenz de Miera,
Proc. Natl. Acad. Sci. U.S.A. 89, 4603-4607, 1992
A:Title: Region-specific expression of a K+ channel gene in brain.
A:Reference number: A45292; MUID:9262488
A:Accession: A45292
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 594-624 <RUD>
A:Note: sequence extracted from NCBI backbone (NCBI:102300, NCBI:102305)
C:Keywords: glycoprotein; ion channel; leucine zipper; transmembrane protein
F:230-248/Domain: transmembrane #status predicted <TM1>
F:282-303/Domain: transmembrane #status predicted <TM2>
F:315-335/Domain: transmembrane #status predicted <TM3>
F:347-365/Domain: transmembrane #status predicted <TM4>
F:382-401/Domain: transmembrane #status predicted <TM5>
F:452-473/Domain: transmembrane #status predicted <TM6>

Query Match 89.9%; Score 71; DB 2; Length 624;
Best Local Similarity 100.0%; Pred. No. 0.00021;

Matches 13: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEHT 13

Db 407 GAOPNDPSASEHT 419

RESULT 7

T34672

probable gntR family transcription regulator - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999

C:Accession: T34672

R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.

submitted to the EMBL Data Library, December 1998

A:Reference number: Z21552

A:Accession: T34672

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-273 <SAU>

A:Cross-references: EMBL:AL034446; PIDN:CAA22393.1; GSPDB:GN00070; SCODEB:SC1A9.23

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCODEB:SC1A9.23

Query Match

Best Local Similarity 65.8%; Score 52; DB 2; Length 273;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEHT 14

Db 43 GAEPDGPARGETH 56

RESULT 8

T16995

probable cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - apple tree

C:Species: Malus domestica (apple tree)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000

C:Accession: T16995

R:Lee, J.R.; An, G.; Kim, S.R.

submitted to the EMBL Data Library, March 1998

A:Description: Molecular characterization of a fruit preferential cDNA encoding a putative

A:Reference number: Z18641

A:Accession: T16995

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-325 <LEF>

A:Cross-references: EMBL:AF053084; NID:q2981474; PID:q2981475

A:Experimental source: cv. Fuji

C:Genetics:

A:Gene: CAD

C:Function:

A:Description: catalyzes the reversible oxidation of cinnamyl alcohol to cinnamylaldehyde

A:Pathway: ligin biosynthesis

C:Superfamily: dihydrokaempferol 4-reductase

C:Keywords: ligin biosynthesis; NADP; oxidoreductase

Query Match

Best Local Similarity 59.5%; Score 47; DB 2; Length 325;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 14

Db 40 PNDPKTEHLH 50

RESULT 9

S13919

potassium channel protein Raw3 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 05-Nov-1999

C:Accession: S13919; S22702

R:Schroeter, K.H.; Ruppersberg, J.P.; Wunder, F.; Rettig, J.; Stocker, M.; Pongs, O.

FEBS Lett. 278, 211-216, 1991

A:Title: Cloning and functional expression of a TEA-sensitive A-type potassium channel

A:Reference number: S13919; MUID:91122287

A:Accession: S13919

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-625 <SCH>

A:Cross-references: EMBL:X62841; NID:q57648; PIDN:CAA44645.1; PID:q57649

R:Rettig, J.; Wunder, F.; Stocker, M.; Lichtenhagen, R.; Mastiaux, F.; Beckh, S.; Ku

EMBO J. 11, 2473-2486, 1992

A:Title: Characterization of a shaw-related potassium channel family in rat brain.

A:Reference number: S22702; MUID:9233159

A:Accession: S22702

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-625 <RET>

A:Cross-references: EMBL:X62841; NID:q57648; PIDN:CAA44645.1; PID:q57649

C:Keywords: glycoprotein; ion channel; leucine zipper; transmembrane protein

F:228-246/Domain: transmembrane #status predicted <TM1>

F:282-303/Domain: transmembrane #status predicted <TM2>

F:315-335/Domain: transmembrane #status predicted <TM3>

F:347-365/Domain: transmembrane #status predicted <TM4>

F:382-401/Domain: transmembrane #status predicted <TM5>

F:452-473/Domain: transmembrane #status predicted <TM6>

F:257,266/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 59.5%; Score 47; DB 2; Length 625;

Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEHT 13

Db 407 GARSPDPRGNDHT 419

RESULT 10

E75613

hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C:Accession: E75613

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.;

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896

A:Accession: E75613

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-214 <MHT>

A:Cross-references: GB:AE001862; GB:AE001825; NID:q6460468; PIDN:AAF12308.1; PID:q646

A:Experimental source: strain R1

C:Genetics:

A:Gene: DRA0170

A:Map position: 2

Query Match

Best Local Similarity 57.0%; Score 45; DB 2; Length 214;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEH 12

Db 129 GAOPQOPAAVEH 140

RESULT 11

S41080

Fri Feb 2 15:15:36 2001

us-09-273-217-3.rpr

Page 5

Job time: 86 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:38:02 ; Search time 45.64 Seconds
(without alignments)
10.489 Million cell updates/sec

Title: US-09-273-217-3

Sequence: 1 GAQPNDBSASEHTH 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq.36.*
1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT.*
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14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT.*
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19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	14	Y42764	Rat potassium chan
2	71	89.9	601	Y34120	Human potassium ch
3	47	59.5	270	R19152	Lung cancer specif
4	47	59.5	274	R19153	Lung cancer specif
5	47	59.5	325	R19151	Lung cancer specif
6	47	59.5	325	R19155	HCAVIII phosphoty
7	47	59.5	354	R19150	Lung cancer specif
8	44	55.7	434	R96419	Peptide fragment o
9	40	50.6	1574	Y84729	Amino acid sequenc
10	39	49.4	338	W15270	Salmonella secreta
11	39	49.4	603	R44004	Basic protease. D
12	39	49.4	1095	P97052	Sequence encoded b

13	39	49.4	1136	9	P82314	Bacillus thuringie
14	39	49.4	1136	10	P93341	Sequence encoded b
15	39	49.4	1178	7	P60051	Sequence of insect
16	39	49.4	2427	21	Y51843	Murine embryo macr
17	38	48.1	98	15	R63235	CNS neural thread
18	38	48.1	98	17	R95914	HR4 human neural t
19	38	48.1	177	18	W13945	Arabidopsis termin
20	38	48.1	202	20	Y35338	Chlamydia pneumoni
21	38	48.1	513	9	P81501	Basic serine prote
22	38	48.1	1788	21	Y85575	D. melanogaster BA
23	38	48.1	2071	21	Y84686	Amino acid sequenc
24	37	46.8	14	21	Y81320	Human growth hormo
25	37	46.8	163	30	Y29213	Amino acid sequenc
26	37	46.8	181	18	W13944	Antirrhinum centro
27	37	46.8	266	20	Y43944	Yeast protein Kina
28	37	46.8	267	20	Y43946	Fission yeast prot
29	37	46.8	285	20	Y34849	Chlamydia pneumoni
30	36	45.6	131	20	Y60109	Human endometrium
31	36	45.6	159	18	W50288	Human Fas antigen
32	36	45.6	160	20	Y48363	Human prostate can
33	36	45.6	246	19	W77312	Polypeptide sequen
34	36	45.6	328	21	Y54617	Arabidopsis Abi4 p
35	36	45.6	376	18	W50287	Human Fas antigen
36	36	45.6	376	19	W60037	Antigenic peptide
37	36	45.6	396	18	W18574	Aggrecanase ariffl
38	36	45.6	396	18	W18575	Aggrecanase ariffl
39	36	45.6	403	20	Y43174	Mouse cyclin E2 pr
40	36	45.6	497	21	Y74865	Neisseria meningit
41	36	45.6	497	21	Y75810	Neisseria meningit
42	36	45.6	497	21	Y75882	Neisseria strain 2
43	36	45.6	507	14	R34538	P/C protein of atc
44	36	45.6	543	16	R79142	Fructosyltransfera
45	36	45.6	584	20	Y29619	Human P1AS3 protei

ALIGNMENTS

RESULT 1
ID Y42764 standard; peptide; 14 AA.
AC Y42764:
XX 20-DEC-1999 (first entry)
XX
XX Rat potassium channel KV3.1 vestibule-derived peptide #3.
DE
XX Ion channel; potassium channel; vestibule; inhibitor; antibody;
KW polyclonal; antagonist; hypertension; cardiac ischemia;
KW bronchial constriction; neurological diseases.
XX
XX Synthetic.
OS Rattus sp.
XX
XX W09948927-A1.
PN
XX 30-SEP-1999.
PD
XX 19-MAR-1999; 99WO-US06019.
PF
XX 25-MAR-1998; 98US-0079268.
PR
XX (CORR) CORNELL RES FOUND INC.
PA
XX Huang X;
PI WPI: 1999-601205/51.
DR Designing specific blockers that bind to the external vestibule region
XX of ion channels, potentially useful for treating e.g. hypertension -
PT Claim 9; Page 8; 40pp; English.
PS

XX This sequence represents a peptide (#3), derived from the
CC extracellular vestibule portion of the rat potassium channel Kv3.1.
CC This was conjugated to keyhole limpet haemocyanin (KLH) and used to
CC generate polyclonal antibodies. The vestibule portion of potassium
CC channels is located on the extracellular portion of the channel protein,
CC and generally comprises a loop between the S5 transmembrane domain and
CC the pore forming region of the channel, or between the pore forming
CC region and the S6 transmembrane domain. The antibodies generated against
CC vestibule peptides act as potassium channel inhibitors by binding to the
CC vestibule portion, physically blocking the pore, or otherwise inducing a
CC conformational change in the channel. These potassium channel blockers
CC are potential therapeutic agents for e.g., hypertension, cardiac
CC ischemia, bronchial constriction and neurological diseases. Such
CC inhibitors are specific for particular types of ion channel, and
CC are produced by rational design based on known nucleotide and amino acid
CC sequences for ion channels.
XX
SQ Sequence 14 AA:

Query Match 100.0%; Score 79; DB 20; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAOPNDPSASEHTH 14
Db 1 gaopndpsasehth 14
|||||

RESULT 2
Y34120 Y34120 standard; Protein; 601 AA.
XX Y34120;
XX 30-NOV-1999 (first entry)
DT Human potassium channel K+Hnov4.
XX
DE
XX
XX Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
XX cardiovascular disorder; CNS disorder; renal disorder.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 103 /note="Ala substituted by Thr in a variant form of
FT K+Hnov4"
XX
XX MO9943696-A1.
XX
XX 02-SEP-1999.
XX
XX 22-FEB-1999; 99MO-US03826.
XX
XX 19-JAN-1999; 99US-0116448.
XX 25-FEB-1998; 98US-0076687.
XX 07-AUG-1998; 98US-0095836.
XX
XX (AXYS-) AXYS PHARM INC.
XX
XX Curran ME, Hu P, Miller AP, Rutter M, Wang J;
XX
XX WPI: 1999-527591/44.
XX N-PSDB; Y34120.
XX
XX New nucleic acids encoding mammalian K+Hnov potassium channel
XX proteins, useful for the diagnosis and treatment of episodic ataxia
XX with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome
XX
XX Claim 3; Page 48-49; 112pp; English.

CC This sequence represents the human K+Hnov4 potassium channel.
CC K+Hnov proteins have a high degree of homology to known potassium
CC channels and may be alpha subunits, which form the functional channel,
CC or accessory subunits that act to modulate the channel activity.
CC K+Hnov4 is a voltage gated potassium channel. K+Hnov cDNAs were
CC isolated by extension of expressed sequence tags (ESTs) which were
CC related but not identical to known human potassium channels. Potential
CC polymorphisms detected as sequence variants between multiple
CC independent clones. Potassium channels have critical roles in various
CC cell types and biochemical pathways. Defective potassium channels are
CC known to cause four human diseases: episodic ataxia with myokymia,
CC cardiac arrhythmia (Long QT syndrome); epilepsy; and Bartter's syndrome.
CC As potassium channels are critical components of virtually all cells,
CC it is likely that abnormal potassium channels are also implicated in
CC certain renal, cardiovascular and central nervous system (CNS) disorders.
CC Nucleotides encoding K+Hnov proteins may be used for identifying
CC homologous or related proteins and the DNA sequences encoding them. They
CC may be used to produce compositions that modulate the expression and
CC function of the K+Hnov protein and in studying the biochemical pathways
CC associated with it. They may also be used for the recombinant production
CC of K+Hnov protein in fermentation cultures. Additionally, such
CC nucleotides may be used in gene therapy protocols for the treatment
CC of diseases associated with abnormal potassium channels.
XX
SQ Sequence 601 AA:

Query Match 89.9%; Score 71; DB 20; Length 601;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAOPNDPSASEHT 13
Db 371 gaopndpsaseht 383
|||||

RESULT 3
R91952 R91952 standard; Protein; 270 AA.
XX
XX R91952;
XX
XX 23-APR-1996 (first entry)
DT Lung cancer specific antigen HCAVIII truncated protein.
XX
XX
XX
XX Non-small cell lung cancer; NSCIC; tumour marker; HCAVIII;
XX carbonic anhydrase; diagnosis; therapy; antibody; ELISA.
XX
XX Synthetic.
XX
XX MO9602552-A1.
XX
XX 01-FEB-1996.
XX
XX 19-JUL-1995; 95MO-US09145.
XX
XX 19-JUL-1994; 94US-0276919.
XX
XX (CYTO-) CYTOCLONAL PHARM INC.
XX
XX Bolion AP, Torczynski RM;
XX
XX WPI: 1996-105844/11.
XX N-PSDB; T15450.
XX
XX Nucleic acid encoding the lung cancer specific antigen HCAVIII -
XX useful for diagnosis and treatment of non-small cell lung cancer
XX
XX Claim 9; Page 53-54; 87pp; English.
XX
XX Truncated forms (R91952-53) of HCAVIII, lacking the membrane spanning
XX fragment and the intracellular domain, were produced in Escherichia

CC cells transformed with a vector carrying the encoding cDNA (see
 CC T15450 and T15451). HCAVIII is a cell surface antigen which is
 CC highly specific for non-small cell lung carcinoma (NSCLC) and which
 CC has features in common with human carbonic anhydrases. The
 CC truncated HCAVIII are more accurate representations of the putative
 CC HCAVIII shed antigen found in biopsy specimens and may be the
 CC preferred antigens for polyclonal antisera and monoclonal antibody
 CC prep. for use in ELISA test development.

XX Sequence 270 AA:

Query Match

Best Local Similarity 59.5%; Score 47; DB 17; Length 270;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
 DB 95 pndpghseht 104

RESULT 4

R91953 R91953 standard; Protein; 274 AA.

XX AC R91953;

DT 23-APR-1996 (first entry)

DE Lung cancer specific antigen HCAVIII truncated protein.

KM Non-small cell lung cancer; NSCLC; tumour marker; HCAVIII;
 KM carbonic anhydrase; diagnosis; therapy; antibody; ELISA.

OS Synthetic.

PN W09602552-A1.

PD 01-FEB-1996.

PF 19-JUL-1995; 95WO-US09145.

PR 19-JUL-1994; 94US-0276919.

PA (CYTO-) CYTOCLONAL PHARM INC.

PI Bolton AP, Torczynski RM;

DR WPI: 1996-105844/11.

DR N-PSDB; T15451.

PT Nucleic acid encoding the lung cancer specific antigen HCAVIII -
 PT useful for diagnosis and treatment of non-small cell lung cancer
 PS Claim 11; Page 56-57; 87pp; English.

CC Truncated forms (R91952-53) of HCAVIII, lacking the membrane spanning
 CC fragment and the intracellular domain, were produced in Escherichia
 CC cells transformed with a vector carrying the encoding cDNA (see
 CC T15450 and T15451). HCAVIII is a cell surface antigen which is
 CC highly specific for non-small cell lung carcinoma (NSCLC) and which
 CC has features in common with human carbonic anhydrases. The
 CC truncated HCAVIII are more accurate representations of the putative
 CC HCAVIII shed antigen found in biopsy specimens and may be the
 CC preferred antigens for polyclonal antisera and monoclonal antibody
 CC prep. for use in ELISA test development.

XX Sequence 274 AA:

Query Match

Best Local Similarity 59.5%; Score 47; DB 17; Length 274;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
 DB 96 pndpghseht 105

RESULT 5

R91951 R91951 standard; Protein; 325 AA.

XX AC R91951;

DT 23-APR-1996 (first entry)

DE Lung cancer specific antigen HCAVIII mature protein.

KM Non-small cell lung cancer; NSCLC; tumour marker; HCAVIII;
 KM carbonic anhydrase; diagnosis; therapy; antibody.

OS Homo sapiens.

PN W09602552-A1.

PD 01-FEB-1996.

PF 19-JUL-1995; 95WO-US09145.

PR 19-JUL-1994; 94US-0276919.

PA (CYTO-) CYTOCLONAL PHARM INC.

PI Bolton AP, Torczynski RM;

DR WPI: 1996-105844/11.

DR N-PSDB; T15449.

PT Nucleic acid encoding the lung cancer specific antigen HCAVIII -
 PT useful for diagnosis and treatment of non-small cell lung cancer
 PS Claim 7; Page 44-46; 87pp; English.

CC The mature HCAVIII protein (R91951) was produced as a GST fusion in
 CC Escherichia coli cells transformed with the encoding cDNA (T15449)
 CC cloned into pGEX4T-1. It was isolated by affinity purification and
 CC thrombin cleavage. HCAVIII is a cell surface antigen which is
 CC highly specific for non-small cell lung cancer, and which shares
 CC regions of homology with human carbonic anhydrases. It can be used
 CC to produce antibodies of therapeutic or diagnostic application.

XX Sequence 325 AA:

Query Match

Best Local Similarity 59.5%; Score 47; DB 17; Length 325;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
 DB 96 pndpghseht 105

RESULT 6
R91955
ID R91955 standard; Protein; 325 AA.
XX
AC R91955;
XX
DT 23-APR-1996 (first entry)
XX
DE HCAVIII phosphorylation-modified (S302G) protein.
XX
KW Non-small cell lung cancer; NSCLC; tumour marker; HCAVIII;
KW carbonic anhydrase; diagnosis; therapy; antibody;
XX phosphorylation.
XX
OS Synthetic.
XX
PN W09602552-A1.
XX
PD 01-FEB-1996.
XX
PE 19-JUL-1995; 95WO-US09145.
XX
PR 19-JUL-1994; 94US-0276919.
XX
PA (CYTO-) CYTOCLONAL PHARM INC.
XX
PI BOLLON AP, Torczynski RM;
XX
DR WPI; 1996-105844/11.
DR N-PSDB; T15454.
XX
PT Nucleic acid encoding the lung cancer specific antigen HCAVIII -
PT useful for diagnosis and treatment of non-small cell lung cancer
XX
PS Claim 16; Page 59-60; 87pp; English.
XX
XX A cDNA sequence (T15454) codes for a phosphorylation-modified form
CC (R91955) of HCAVIII, a cell surface antigen which is highly
CC specific for non-small cell lung carcinoma (NSCLC) and which has
CC features in common with human carbonic anhydrases. The modified
CC HCAVIII has glycine substituted for serine at position 302 of the
CC mature protein. It is used to study the role of HCAVIII serine
CC phosphorylation in oncogenesis.
XX
SQ Sequence 325 AA;

Query Match 59.5%; Score 47; DB 17; Length 325;
Best Local Similarity 80.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
| | | | |
Db 96 pndpghseht 105

RESULT 7
R91950
ID R91950 standard; Protein; 354 AA.
XX
AC R91950;
XX
DT 23-APR-1996 (first entry)
XX
DE Lung cancer specific antigen HCAVIII pre-protein.
XX
KW Non-small cell lung cancer; NSCLC; tumour marker; HCAVIII;
KW carbonic anhydrase; diagnosis; therapy; antibody.
XX
OS Homo sapiens.
XX

EH Key Location/Qualifiers
FT Modified-site 28
FT /label= N-glycosylation_site
FT Peptide 1..29
FT /label= sig_peptide
FT Protein 30..354
FT /label= Mat_protein
FT Modified-site 80
FT /label= N-glycosylation_site
FT Modified-site 162
FT /label= N-glycosylation_site
FT Modified-site 180
FT /label= N-glycosylation_site
FT Modified-site 231
FT /label= N-glycosylation_site
FT Modified-site 328..331
FT /label= Phosphorylation_site
FT /note= "the phosphorylation site recognised by
FT protein kinase C and other kinases"

W09602552-A1.
01-FEB-1996.
19-JUL-1995; 95WO-US09145.
19-JUL-1994; 94US-0276919.
(CYTO-) CYTOCLONAL PHARM INC.
BOLLON AP, Torczynski RM;
WPI; 1996-105844/11.
N-PSDB; T15448.
Nucleic acid encoding the lung cancer specific antigen HCAVIII -
useful for diagnosis and treatment of non-small cell lung cancer
Claim 1; Page 41-42; 87pp; English.
The pre-protein (R91950) of a cell surface antigen highly specific
for non-small cell lung carcinoma, HCAVIII, is the product of a
cDNA sequence (T15448) in vector pLC56. HCAVIII has some features
in common with 7 previously known human carbonic anhydrases.
The HCAVIII mature protein (R91951) and truncated HCAVIII lacking
the transmembrane domain (R91952-53) have been expressed in
Escherichia coli and used to raise antibodies for diagnostic and
therapeutic applications.

Query Match 59.5%; Score 47; DB 17; Length 354;
Best Local Similarity 80.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
| | | | |
Db 125 pndpghseht 134

RESULT 8
R96419
ID R96419 standard; peptide; 434 AA.
XX
AC R96419;
XX
DT 11-NOV-1996 (first entry)
XX
DE Peptide fragment of N-type calcium channel.
XX
KW Calcium channel; synapse; synaptic vesicle; presynaptic; syntaxin;
KW synaptosome; neuronal cell death; ishaemia; stroke; epilepsy;
KW

KW	cognitive deficit; inhibition; screening; detection; treatment.
XX	
OS	Rattus rattus.
XX	
FT	Key Location/Qualifiers
FT	Region 718..1141
XX	/note= "Claimed peptide region."
PN	MO9615149-A2.
XX	
PD	23-MAY-1996.
XX	
PE	09-NOV-1995; 95WO-US14776.
XX	
PR	10-NOV-1994; 94US-0337602.
XX	
PA	(UNIM) UNIV WASHINGTON.
PI	Catterall WA, Sheng Z;
XX	
DR	WPJ; 1996-259782/26.
XX	
PT	Screening for presynaptic calcium channel blockers - identifies
PT	compounds which inhibit docking of presynaptic vesicles to calcium
PT	channels, rather than compounds which inhibit calcium influx
XX	
PS	Claim 7; Figure 11A; 53pp; English.
XX	
CC	A method of screening for compounds that inhibit the interaction
CC	between presynaptic calcium channels and presynaptic vesicles
CC	comprises contacting calcium channel-like peptide with a candidate
CC	compound under conditions sufficient to permit binding between the
CC	peptide and the candidate compound, where the peptide is able to
CC	bind syntaxin or synaptosome associated protein, and then detecting
CC	the presence or absence of binding between the peptide and the
CC	candidate compound, thereby determining whether the candidate
CC	compound bound to the peptide. The method allows for the screening
CC	of compounds which inhibit the docking of presynaptic vesicles to
CC	calcium channels and which therefore prevent neurotransmitter release
CC	by binding to a selected presynaptic calcium channel-like peptide.
CC	Isolated compounds may be used in the prevention of neuronal cell
CC	death that accompanies cerebral ischemia. They may also be used in
CC	the treatment of stroke, cognitive deficit related to cardiac
CC	surgery and neuronal damage caused during acute epileptic episodes.
CC	This sequence corresponds to the LII-III loop (amino acids 710-1143
CC	of the rat N-type calcium channel.
XX	
SQ	Sequence 434 AA;
	Query Match 55.7%; Score 44; DB 17; Length 434;
	Best Local Similarity 58.3%; Pred. No. 9.1';
	Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY	1 GAOPNDPSASEH 12
	I::I::I::I : I
DB	357 gsqpsdpstvh 368
RESULT 9	
ID Y84729	Y84729 standard; Protein: 1574 AA.
XX AC	Y84729;
XX DT	08-AUG-2000 (first entry)
XX DE	Amino acid sequence of FK-520 PKs gene cluster module 8.
KW FK-520:	polyketide synthase; PKS; gene cluster; immunosuppressant;
KW immunophilin; FK-506	binding protein; polyketide compound; uvelitis;
KW transplant rejection;	graft-versus-host disease; alopecia universalis;
KW autoimmune chronic active	hepatitis; inflammatory bowel disease;

KW	multiple sclerosis; primary biliary cirrhosis; scleroderma;
KW	neurite outgrowth; nerve regrowth; Parkinson's disease;
KW	Alzheimer's disease; stroke; traumatic spinal cord; brain injury;
KW	peripheral neuropathy.
XX	
OS	Streptomyces hygroscopicus.
XX	
PN	W0200020601-A2.
XX	
PD	13-APR-2000.
XX	
PE	01-OCT-1999; 99WO-US22886.
XX	
PR	02-OCT-1998; 98US-0102748.
PR	11-MAR-1999; 99US-0123810.
XX	
PR	17-JUN-1999; 99US-0139650.
XX	
PA	(KOSA-) KOSAN BIOSCIENCES INC.
XX	
PI	Reeves C, Chu D, Khosla C, Santl D, Wu K;
XX	
DR	WPI; 2000-317716/27.
DR	N-PSDB; A14665.
XX	
PT	New isolated polyketide synthase nucleic acid and polyketide compounds,
PT	useful for treating e.g. transplant rejection, uveitis, multiple
PT	sclerosis, Alzheimer's disease, Parkinson's disease, stroke, or
PT	peripheral neuropathy -
XX	
PS	Example 2; Page 90-93; 126pp; English.
XX	
CC	The present sequence represents module 8 of the FK-520 polyketide
CC	synthase (PKS) gene cluster of strain MA6548. FK-506 is a potent
CC	immunosuppressant, and acts through initial formation of an
CC	intermediate complex with protein immunophilins known as FK-506
CC	binding proteins. The nucleic acids are used for producing polyketide
CC	compounds. The polyketide compounds can be used as immunosuppressants to
CC	prevent or treat transplant rejection, graft-versus-host disease or
CC	uveitis. They can also be used for treating e.g. alopecia universalis,
CC	autoimmune chronic active hepatitis, inflammatory bowel disease,
CC	multiple sclerosis, primary biliary cirrhosis, or scleroderma. They
CC	also have neurotrophic activity and can be used to promote neurite
CC	outgrowth in NGF-treated PC12 cells and in sensory neuronal cultures,
CC	and in intact animals, they promote regrowth of damaged facial and
CC	sciatic nerves, and repair lesioned serotonin and dopamine neurons in
CC	the brain. They can also be used for treating e.g. Parkinson's disease,
CC	Alzheimer's disease, stroke, traumatic spinal cord and brain injury, or
CC	peripheral neuropathies. They can also be used in agricultural and
CC	veterinary applications.
XX	
XX	
SQ	Sequence 1574 AA;
XX	
QY	4 PNDPSASEHT 13
QY	1111: 1111
DB	722 pndptrsqht 731
XX	
RESULT 10	
W15270	
ID	W15270 standard; Protein: 338 AA.
XX	
AC	W15270;
XX	
DT	04-AUG-1997 (first entry)
XX	
DE	Salmonella secreted protein SspD.
XX	
KW	Salmonella secreted protein; SspD; bacterial-mediated endocytosis;

KM diagnosis: therapy: vaccine: attenuation: virulence.
 XX
 OS Salmonella typhimurium.
 XX
 FH Key
 FT 1.338 Location/Qualifiers
 FT /note= "the amino acid sequence does not fully
 FT correspond to the translated sequence of
 FT the sspD gene of Fig 21"
 XX
 PN M09718225-A1.
 XX
 PD 22-MAY-1997.
 XX
 PE 14-NOV-1996; 96WO-US18504.
 XX
 PR 14-NOV-1995; 95US-0006733.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Miller SI.
 XX
 DR WPI: 1997-289217/26.
 DR N-PSDB: T67030.
 XX
 PT New isolated Salmonella secreted proteins and related genes - used
 PT to develop products for the detection, treatment or prevention of
 PT Salmonella infections
 XX
 PS Claim 24; Fig 14; 95pp; English.
 XX
 CC Salmonella secreted proteins SspB, SspC, SspD and SspA (W15268-71)
 CC are virulence factors involved (except SspA) in bacterial
 CC mediated endocytosis, and are able to translocate into human
 CC epithelial cells. Ssp secretion is dependent on the expression
 CC of *prgH* (see also T67036). Ssp genes (T67028-31) were isolated
 CC by examining *S. typhimurium* mutants in invasion assays on HEP-2
 CC epithelial cells. Ssp polypeptides can be used in methods for the
 CC detection, treatment or prevention of Salmonella infection.
 CC Chemeric proteins incorporating Ssp can be used to target an
 CC antigen to epithelial cells or to induce a cytotoxic T cell
 CC response in a mammal. Decreased secretion of Ssp provides
 CC attenuated bacterial cells suitable as live vaccines.
 XX
 SQ Sequence 338 AA;
 Query Match 49.4%; Score 39; DB 18; Length 338;
 Best Local Similarity 70.0%; Pred. No. 49;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 3 QPNDSASEH 12
 : | | | | | | |
 Db 19 rpgpsaseh 28
 RESULT 11
 ID R44004 standard: Protein; 603 AA.
 XX
 AC R44004;
 XX
 DT 13-MAY-1994 (first entry)
 XX
 DE Basic protease.
 XX
 KM Acid protease; isoenzyme; D. nodosus; benign; strain 305; epitope; VI;
 KM basic protease; diagnosis; detection; virulent; intermediate; vaccine;
 KM antibody; V2; G100P1; B2; foot rot; detergent; domestic; dairy; food;
 KM textile; leather; pharmaceutical; medical; cosmetic; veterinary.
 XX
 OS Dichelobacter nodosus benign strain 305.

PN GB2267148-A.
 XX
 PD 24-NOV-1993.
 XX
 PE 04-MAY-1993; 93GB-0009159.
 XX
 PR 01-MAY-1992; 92AU-0002226.
 PR 10-JUL-1992; 92AU-0003445.
 PR 14-SEP-1992; 92AU-0004708.
 PR 14-SEP-1992; 92AU-0004711.
 PR 10-DEC-1992; 92AU-0006284.
 PR 14-JAN-1993; 93AU-0006827.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Edwards RD, Focareta A, Kortt AA, Lilley GG, Riffkin MC;
 PI Stewart DJ, Vaughan JA, Wang L, Wang LF;
 XX
 DR WPI: 1993-353826/45.
 DR N-PSDB: Q51275.
 XX
 PT Ovine foot rot infection diagnostic assay for rapid strain
 PT differentiation - by detecting epitope(s) and/or antibodies
 PT specific to epitope in virulent, benign, and/or intermediate
 PT strains, for protease vaccine and deoxyribonucleic acid
 XX
 PS Claim 36; Fig 4; 103pp; English.
 XX
 CC This sequence represents the basic protease from the D.
 CC nodosus benign strain 305. Epitopes found on acidic or basic
 CC proteases may be used in the diagnostic method of the invention.
 CC The method involves detecting at least one of:
 CC (i) an epitope present in virulent and/or at least some
 CC intermediate strains but not in benign strains;
 CC (ii) an epitope present in benign and/or at least some
 CC intermediate strains but not in virulent strains;
 CC (iii) an epitope present in some intermediate strains but not
 CC in virulent, or most benign strains; or
 CC (iv) antibodies specific to these epitopes.
 CC Epitopes in class (i) are pref. present on V2 or G100P1, class (ii)
 CC are pref. present on B2 and class (iii) are pref. present on V1. D.
 CC nodosus proteases are useful in vaccines for the control of foot rot,
 CC eg. as an additive to known vaccines based on basic proteases. Hybrid
 CC proteases can serve as carriers of foreign epitopes. The proteases
 CC can be used as detergents for domestic, dairy, food, textile, leather,
 CC pharmaceutical, medical, cosmetic and veterinary purposes.
 XX
 SQ Sequence 603 AA;
 Query Match 49.4%; Score 39; DB 14; Length 603;
 Best Local Similarity 53.8%; Pred. No. 94;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 OY 2 AOPNDPSASEH 14
 : | | | | | : |
 Db 133 aapndpsyqgwh 145
 RESULT 12
 ID P97052 standard: protein; 1095 AA.
 XX
 AC P97052;
 XX
 DT 23-DEC-1990 (first entry)
 XX
 DE Sequence encoded by insecticide gene from *Bacillus thuringiensis*
 DE israelensis strain.
 XX
 KM Insecticide; diptera larvae; aedes.
 XX
 OS *Bacillus thuringiensis*.

XX JP01080294-A.
 PN 27-MAR-1989.
 PD 21-SEP-1987; 87JP-0238394.
 PF 21-SEP-1987; 87JP-0238394.
 PR 21-SEP-1987; 87JP-0238394.
 PA (MARU-) MARUBENI KK.
 PA (SUMO) SUMITOMO CHEMICAL IND. KK.
 DR WPI: 1989-134798/18.
 DR N-PSDB: N92515.
 XX Insecticide protein gene -
 PT from *Bacillus thuringiensis israelensis* strain, used to produce
 PT protein toxic to diptera larvae, e.g. aedes
 PS Disclosure: Fig 2-1 to 2-3; 8pp; Japanese.
 CC The protein gene has high insecticide activity to diptera
 CC larvae such as aedes.
 CC Sequence 1095 AA;
 SQ

Query Match 49.4%; Score 39; DB 10; Length 1095;
 Best Local Similarity 45.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASERTH 14
 ||| : ::||
 Db 392 pnpqtvndyth 402

RESULT 13
 P82314
 ID P82314 standard; protein; 1136 AA.
 AC P82314;
 XX 13-NOV-1990 (first entry)
 DT 13-NOV-1990 (first entry)
 XX *Bacillus thuringiensis* 8 protein.
 DE *Bacillus thuringiensis* 8 protein.
 XX Bt 8 protein; insecticides; mosquitos.
 KM W08806631-A.
 PN 07-SEP-1988.
 XX 07-SEP-1988.
 PD 03-MAR-1988; 88WO-US00734.
 PF 03-MAR-1988; 88WO-US00734.
 XX 04-MAR-1987; 87US-0021405.
 PR 04-MAR-1987; 87US-0021405.
 XX (UNMS) MICHIGAN STATE UNIV.
 PA (PLAN-) PLANT GENETIC SYST.
 PA (UNMI) UNIV OF MICHIGAN.
 XX Vaecck MA, Chungjatupornchai W, McIntosh L;
 PI WPI: 1988-271170/38.
 DR N-PSDB: N92106.
 DR Chimeric gene for expression in *Cyanobacteria* - contg. DNA fragment
 PT coding for insecticidal active protein produced by *Bacillus* strain.
 PT coding for insecticidal active protein produced by *Bacillus* strain.
 XX Disclosure: ; P; English.
 PS The corresp. gene is ligated to a promoter region enabling ex-
 CC pression in *Cyanobacteria* and the resultant chimeric gene is used
 CC to produce this Bt 8 protein. A truncated form of the protein can

CC also be produced using a shorter gene. Transformed *Cyanobacteria*
 CC and their progeny can be used in insecticidal compsns., esp. for
 CC controlling mosquitos.
 CC Sequence 1136 AA;
 SQ

Query Match 49.4%; Score 39; DB 9; Length 1136;
 Best Local Similarity 45.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASERTH 14
 ||| : ::||
 Db 433 pnpqtvndyth 443

RESULT 14
 P93341
 ID P93341 standard; protein; 1136 AA.
 AC P93341;
 XX 27-JAN-1991 (first entry)
 DT 27-JAN-1991 (first entry)
 XX Sequence encoded by toxin gene derived from a *Bacillus thuringiensis* var.
 DE israelensis (B.t.i.) microbe identified as strain HD567.
 XX Insecticide; diptera; mosquito.
 KM *Bacillus thuringiensis*.
 OS *Bacillus thuringiensis*.
 XX EP308199-A.
 PN 22-MAR-1989.
 PD 14-SEP-1988; 88EP-0308498.
 PF 14-SEP-1988; 88EP-0308498.
 XX 16-JUN-1988; 88US-0207690.
 PR 16-JUN-1988; 88US-0207690.
 XX (MYCO-) MYCOGEN CORP.
 PA Gilroy TE;
 XX WPI: 1989-087579/12.
 DR N-PSDB: N91003.
 XX *Bacillus thuringiensis* toxin toxic to dipteran insects -
 PT produced by gene isolated from *Bacillus thuringiensis* var.
 PT israelensis strain
 XX Claim 1; pp 7-10; 13pp; English.
 PS A toxin active against dipteran insects, having a specified aa sequence
 CC or a mutant having the same protein secondary structure or, if the
 CC structure is altered, having the same biological activity, is claimed.
 CC Also claimed is a DNA molecule including a nucleotide sequence encoding
 CC the aa sequence. The novel toxin gene is toxic to dipteran insects e.g.
 CC mosquitos.
 CC Sequence 1136 AA;
 SQ

Query Match 49.4%; Score 39; DB 10; Length 1136;
 Best Local Similarity 45.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASERTH 14
 ||| : ::||
 Db 433 pnpqtvndyth 443

RESULT 15
 P60051

ID P60051 standard; Protein; 1178 AA.
XX
AC P60051;
XX
DT 06-SEP-1991 (first entry)
XX
DE Sequence of insecticidal protein related to bacterial delta
DE endotoxin encoded by VB131 clone circular plasmid obtained from
DE the Bacillus thuringiensis var. israelensis.
XX
KW Insecticide; microbial.
XX
OS Bacillus thuringiensis.
XX
PN EP195285-A.
XX
PD 24-SEP-1986.
XX
PE 27-FEB-1986; 86EP-0102547.
XX
PR 28-FEB-1985; 85US-0706836.
XX
PA (UYGE-) UNIV GEORGIA RES.
XX
PI Sekar VS, Carlton BD;
XX
DR WPI; 1986-253299/39.
XX
DR N-PSDB; N60055.
XX
PT Insecticidal protein related to bacterial delta-endotoxin - is
PT obtd. by recombinant DNA methods from transform microorganism
XX
PS Claim 28; Fig 8; 69pp; English.
XX
CC The patentors claim a toxic protein having an amino portion
CC identical to the amino portion of delta-endotoxin from Bacillus
CC thuringiensis var. israelensis and a carboxy-terminus portion
CC different from the carboxy portion of the delta-endotoxin. The
CC protein has the toxic properties of the delta-endotoxin. Appln. is
CC at 0.2-10 x 1,000,000,000 I.U./acre.
XX
SQ Sequence 1178 AA;

Query Match 49.4%; Score 39; DB 7; Length 1178;
Best Local Similarity 45.5%; Pred. No. 2e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 PNDPASEH7H 14
II|: ::||
Db 432 pndpaseh7h 442

Search completed: February 2, 2001, 10:38:03
Job time: 136 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 2, 2001, 10:41:50 ; Search time 20.39 Seconds

(without alignments)
23.757 Million cell updates/sec

Title: US-09-273-217-4

Perfect score: 78

Sequence: 1 FAEDDPTSGFSSIP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

88757

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	523	1	PI22001 homo sapien
2	71	91.0	523	1	PI5384 rattus norv
3	71	91.0	528	1	PI6390 mus musculu
4	59	75.6	653	1	P22459 homo sapien
5	59	75.6	654	1	O61423 mus musculu
6	59	75.6	654	1	Q28527 mustela put
7	59	75.6	655	1	PI5385 rattus norv
8	59	75.6	660	1	Q05037 bos taurus
9	49	62.8	529	1	PI7658 homo sapien
10	49	62.8	602	1	PI9024 rattus norv
11	48	61.5	495	1	Q09470 homo sapien
12	48	61.5	495	1	PI6388 mus musculu
13	48	61.5	495	1	PI4099 rattus norv
14	48	61.5	530	1	PI7659 rattus norv
15	48	61.5	601	1	P79197 mustela put
16	47	60.3	598	1	P50638 oryctolagus
17	47	60.3	613	1	P22460 homo sapien
18	46	59.0	499	1	PI6389 mus musculu
19	46	59.0	499	1	PI5386 mus musculu
20	46	59.0	499	1	P22739 xenopus lae
21	45	57.7	415	1	P73368 homo sapien
22	44	56.4	602	1	Q61762 mus musculu
23	43	55.1	597	1	P10122 bos taurus
24	42	53.8	334	1	P10182 herpes simp
25	42	53.8	802	1	O62959 rattus norv
26	42	53.8	806	1	O62959 rattus norv
27	41	52.6	78	1	PI6511 conus texti
28	41	52.6	414	1	Q62762 rattus norv
29	41	52.6	575	1	Q08101 bovine herp
30	40	51.3	273	1	Q09081 oryctolagus
31	40	51.3	330	1	Q09940 bacillus su
32	40	51.3	446	1	Q17239 bombyx mori
33	40	51.3	742	1	PI5835 homo sapien

ALIGNMENTS

RESULT	ID	SEQUENCE	STANDARD	PRT	AA
1	CIK3_HUMAN				
2	PI22001				
3	01-AUG-1991 (Rel. 19, Created)				
4	01-NOV-1995 (Rel. 32, Last sequence update)				
5	30-MAY-2000 (Rel. 39, Last annotation update)				
6	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.3 (HPCN3) (HGK5) (HUKIII)				
7	(HLK3).				
8	KCNK3 OR HGK5.				
9	Homo sapiens (Human).				
10	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
11	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
12	SEQUENCE FROM N.A.				
13	TISSUE=LYMPHOCYTES;				
14	MEDLINE=92189730; PubMed=1547020;				
15	Cai Y.-C., Osborne P.B., North R.A., Dooley D.C., Douglass J.;				
16	Characterization and functional expression of genomic DNA encoding				
17	the human lymphocyte type n potassium channel.*;				
18	DNA Cell Biol. 11:163-172(1992).				
19	[3]				
20	SEQUENCE FROM N.A.				
21	MEDLINE=92235098; PubMed=1373731;				
22	Attali B., Romey G., Honore E., Schmid-Alliana A., Mattel M.-G.,				
23	Lesage F., Ricard P., Barhanin J., Lazdunski M.;				
24	Cloning, functional expression, and regulation of two K+ channels in				
25	human T lymphocytes.*;				
26	J. Biol. Chem. 267:8650-8657(1992).				
27	[4]				
28	SEQUENCE FROM N.A.				
29	TISSUE=BLD;				
30	MEDLINE=95130104; PubMed=7829094;				
31	Folander K., Douglass J., Swanson R.;				
32	Confirmation of the assignment of the gene encoding Kvl.3, a				
33	voltage-gated potassium channel (KCNK3) to the proximal short arm of				
34	human chromosome 1.*;				
35	Genomics 23:295-296(1994).				
36	ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED				
37	CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE				
38	MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH				
39	WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL				
40	GRADIENT.				
41	-I- SUBUNIT: HETEROPTRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).				
42	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
43	-I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE				

CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: M55515; AAA36425.1; -
 CC EMBL: M38217; AAB88073.1; -
 CC EMBL: M85217; AAA59457.1; -
 CC EMBL: L23499; AAC31761.1; -
 CC HSSP: P03621; 2IFN.
 CC MIM: 176263; -
 CC INTERPRO: IPR000636; -
 CC INTERPRO: IPR003091; -
 CC PRAM: PF00520; Ion_trans; 1.
 CC PRINTS: PR00169; KCHANNEL.
 CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycoprotein; Multigene family; Phosphorylation.
 CC FT TRANSMEM 183 201 SEGMENT S1.
 CC FT TRANSMEM 243 264 SEGMENT S2.
 CC FT TRANSMEM 276 296 SEGMENT S3.
 CC FT TRANSMEM 311 329 SEGMENT S4.
 CC FT TRANSMEM 346 365 SEGMENT S5.
 CC FT TRANSMEM 407 429 SEGMENT S6.
 CC FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT MOD_RES 468 468 PHOSPHORYLATION (BY CARK)
 CC FT MOD_RES 468 468 (POTENTIAL).
 CC FT CONFLICT 20 20 A -> G (IN REF. 1).
 CC FT CONFLICT 37 37 L -> V (IN REF. 1).
 CC FT CONFLICT 61 61 L -> V (IN REF. 3).
 CC FT CONFLICT 91 91 L -> V (IN REF. 1).
 CC FT CONFLICT 257 257 E -> K (IN REF. 4).
 CC FT CONFLICT 338 338 T -> S (IN REF. 1).
 CC FT CONFLICT 419 419 T -> S (IN REF. 1).
 CC FT CONFLICT 488 488 S -> T (IN REF. 1).
 CC SO SEQUENCE 523 AA; 58303 MW; 8BA2F1C7C802BA11 CRC64;

Query Match 100.0%; Score 78; DB 1; Length 523;
 Best local Similarity 100.0%; Pred. No. 6; 7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FARADPTSGFSIP 15
 DB 366 FARADPTSGFSIP 380

RESULT 2
 C1K3_RAT STANDARD; PRT; 525 AA.
 ID C1K3_RAT
 AC P15384;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (RGK5) (RCK3) (KV3).
 GN KCNA3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;
 RX MEDLINE=90059914; Pubmed=2555158;
 RA Stuehmer W., Ruppersberg J.P., Schroeter K.H., Sakmann B.,
 RA Stocker M., Giese K.P., Perschke A., Baumann A., Pongs O.;
 RT "Molecular basis of functional diversity of voltage-gated potassium
 RT channels in mammalian brain.";
 RL EMBO J. 8:3235-3244(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=90297965; Pubmed=2361015;
 RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B.,
 RA Foldner K., Luneau C.J., Antanavage J., Oliva C., Bunrow S.A.,
 RA Bannett C., Stein R.B., Kaczmarek L.M.;
 RT "Cloning and expression of cDNA and genomic clones encoding three
 RT delayed rectifier potassium channels in rat brain.";
 RL Neuron 4:929-939(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LYMPHOCYTES;
 RX MEDLINE=90278098; Pubmed=2351830;
 RA Douglass J., Osborne P.B., Cai Y.C., Wilkinson M., Christie M.J.,
 RA Adelman J.P.;
 RT "Characterization and functional expression of a rat genomic DNA
 RT clone encoding a lymphocyte potassium channel.";
 RL J. Immunol. 144:4841-4850(1990).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: X16001; CAA34132.1; -
 CC EMBL: M30312; AAA42035.1; -
 CC EMBL: M31744; AAA41500.1; -
 CC DR PIR: S06708; S06708.
 CC DR PIR: JH0168; JH0168.
 CC DR HSSP: P03621; 2IFN.
 CC DR INTERPRO: IPR000636; -
 CC DR INTERPRO: IPR003091; -
 CC DR PRAM: PF00520; Ion_trans; 1.
 CC DR PRINTS: PR00169; KCHANNEL.
 CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycoprotein; Multigene family; Phosphorylation.
 CC FT TRANSMEM 185 203 SEGMENT S1.
 CC FT TRANSMEM 245 266 SEGMENT S2.
 CC FT TRANSMEM 278 298 SEGMENT S3.
 CC FT TRANSMEM 313 331 SEGMENT S4.
 CC FT TRANSMEM 348 367 SEGMENT S5.
 CC FT TRANSMEM 409 431 SEGMENT S6.
 CC FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT MOD_RES 470 470 PHOSPHORYLATION (BY CAPK)
FT CONFLICT 106 106 (POTENTIAL)
FT CONFLICT 181 181 F -> L (IN REF. 1)
FT CONFLICT 430 430 G -> R (IN REF. 3)
FT CONFLICT 430 430 V -> L (IN REF. 3)
SQ SEQUENCE 525 AA: 58424 MW: 6DA869D5471C401 CRC64:

Query Match 91.0%; Score 71; DB 1; Length 525;
Best Local Similarity 86.7%; Pred. No. 0.00011;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAADDPSTSGFSSIP 15
Db 368 FAADDPSSGFNSIP 382

RESULT 3
CIRK3_MOUSE
ID CIRK3_MOUSE STANDARD: PRT: 528 AA.
AC P16390.
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.3 (MK3).
GN KCNA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RP MEDLINE-90161996; PubMed-2305265;
RA Chandry K.G., Williams C.B., Spencer R.H., Aguilar B.A.,
RA Ghanshani S., Tempel B.L., Gutan G.A.;
RT "A family of three mouse potassium channel genes with intronless
RT coding regions.";
RT Science 247:973-975(1990).
RL
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC -----
CC EMBL: M30441; AAA39716.1; -
CC HSSP: P03621; 2IFN.
CC MGS: MGI:96660; KCNA3.
CC INTERPRO: IPR000636; -
CC INTERPRO: IPR003091; -
CC PFM: PF00520; Ion_trans. 1.
CC PRINTS: PR00169; KCHANNEL.
CC Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 188 206 SEGMENT S1.

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FT TRANSMEM 248 269 SEGMENT S2.
FT TRANSMEM 281 301 SEGMENT S3.
FT TRANSMEM 316 334 SEGMENT S4.
FT TRANSMEM 351 370 SEGMENT S5.
FT TRANSMEM 412 434 SEGMENT S6.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 473 473 PHOSPHORYLATION (BY CAPK)
SQ SEQUENCE 528 AA: 58526 MW: CBD65F1515F9A731 CRC64:

Query Match 91.0%; Score 71; DB 1; Length 528;
Best Local Similarity 86.7%; Pred. No. 0.00011;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAADDPSTSGFSSIP 15
Db 371 FAADDPSSGFNSIP 385

RESULT 4
CIRK4_HUMAN
ID CIRK4_HUMAN STANDARD: PRT: 653 AA.
AC P22459.
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.4 (HK1) (HPCN2) (HBK4)
DE (HUK11).
GN KCNA4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP MEDLINE-91095456; PubMed-1986382;
RA Philipson L.H., Hice R.E., Schaefer K., Lamendola J., Bell G.I.,
RA Nelson D.J., Steiner D.F.;
RT "Sequence and functional expression in Xenopus oocytes of a human
RT insulinoma and islet potassium channel.";
RT Proc. Natl. Acad. Sci. U.S.A. 88:53-57(1991).
RL
RN [2]
RP SEQUENCE FROM N.A.
RP TISSUE-SKELETAL MUSCLE;
RX MEDLINE-91095456; PubMed-1986382;
RA Philipson L.H., Hice R.E., Schaefer K., Lamendola J., Bell G.I.,
RA Nelson D.J., Steiner D.F.;
RT "Sequence of a human fetal skeletal muscle potassium channel cDNA
RT related to RCK4.";
RT Nucleic Acids Res. 18:7160-7160(1990).
RN [3]
RP SEQUENCE FROM N.A.
RP TISSUE-HEART;
RX MEDLINE-91160866; PubMed-2001794;
RA Tamkun M.M., Kloth K.M., Walbridge J.A., Kroemer H., Roden D.M.,
RA Glover D.M.;
RT "Molecular cloning and characterization of two voltage-gated K+
RT channel cDNAs from human ventricle.";
RL FASEB J. 5:331-337(1991).
RN [4]
RP SEQUENCE FROM N.A.
RP TISSUE-BRAIN;
RA Ramaswami M., Gautam M., Kamb A., Rudy B., Tanouye M.A.,
RA Mathew M.K.;
RT "Human potassium channel genes: molecular cloning and functional
RT expression.";
RL Mol. Cell. Neurosci. 1:214-223(1990).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH

```

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CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC -----
DR EMBL: M55514: AAA60034.1: -.
DR EMBL: M60450: AAA61275.1: -.
DR EMBL: L02751: AAA36140.1: -.
DR PIR: S12630: S12630.
DR HSSP: P15385: 12TO.
DR MIM: 176266: -.
DR INTERPRO: IPR000636: -.
DR INTERPRO: IPR003091: -.
DR PFAM: PF00520: Ion_trans; 1.
DR PRINTS: PR00169: KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
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CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
FT TRANSSEM 308 326 SEGMENT S1 (POTENTIAL).
FT TRANSSEM 371 392 SEGMENT S2 (POTENTIAL).
FT TRANSSEM 404 424 SEGMENT S3 (POTENTIAL).
FT TRANSSEM 443 461 SEGMENT S4 (POTENTIAL).
FT TRANSSEM 478 497 SEGMENT S5 (POTENTIAL).
FT TRANSSEM 539 561 SEGMENT S6 (POTENTIAL).
FT DOMAIN 62 65 POLY-HIS.
FT DOMAIN 123 137 POLY-GLU.
FT DOMAIN 162 165 POLY-GLY.
FT DOMAIN 433 436 POLY-GLN.
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 90 90 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 599 599 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 599 599 PHOSPHORYLATION (BY CAPK)
FT CONFLICT 38 38 R -> A (IN REF. 3 AND 4).
FT CONFLICT 42 42 R -> A (IN REF. 3 AND 4).
FT CONFLICT 84 88 EEEAT -> RRRRO (IN REF. 3 AND 4).
FT CONFLICT 304 304 D -> S (IN REF. 3 AND 4).
FT CONFLICT 542 542 V -> S (IN REF. 3 AND 4).
FT CONFLICT 631 631 A -> G (IN REF. 3 AND 4).
SQ SEQUENCE 653 AA: 73288 MW: 7A66781B827D6F27 CRC64:

```

Query Match 75.6% Score 59; DB 1; Length 653;
 Best Local Similarity 73.3% Pred. No. 0.015; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAADPTGSSP 15
 |||||:|:|:|
 Db 498 FAADPTGSSP 512

RESULT 5
 CIRK MOUSE STANDARD; PRT: 654 AA.
 ID 061423;
 DT 15-JUL-1998 (Rel. 36, Created)

```

DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL4.4.
GN KCNA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AKR:
RX MEDLINE-94297198: Pubmed-8020965.
RA Wmoyre R.S., Kosenberg J.R., Kinoshita K.D., Alyar J., Coyne C.,
RA Chen X.N., Hustad C.M., Copeland N.G., Gutman G.A., Jenkins N.A.,
RA Chandy K.G.;
RT "Genomic organization, nucleotide sequence, biophysical properties,
RT and localization of the voltage-gated K+ channel gene KCNA4/Kv1.4 to
RT mouse chromosome 2/human 11p14 and mapping of KCNC1/Kv3.1 to mouse
RT 7/human 11p14.3-p15.2 and KCNA1/Kv1.1 to human 12p13."
RL Genomics 20:191-202(1994).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U03723: AAB60668.1: -.
DR HSSP: P15385: 12TO.
DR MIM: 176266: -.
DR MED: M61:96661: KCNA4.
DR INTERPRO: IPR000636: -.
DR INTERPRO: IPR003091: -.
DR PFAM: PF00520: Ion_trans; 1.
DR PRINTS: PR00169: KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSSEM 309 327 SEGMENT S1 (POTENTIAL).
FT TRANSSEM 372 393 SEGMENT S2 (POTENTIAL).
FT TRANSSEM 405 425 SEGMENT S3 (POTENTIAL).
FT TRANSSEM 444 462 SEGMENT S4 (POTENTIAL).
FT TRANSSEM 479 498 SEGMENT S5 (POTENTIAL).
FT TRANSSEM 540 562 SEGMENT S6 (POTENTIAL).
FT DOMAIN 38 50 POLY-ALA.
FT DOMAIN 62 65 POLY-HIS.
FT DOMAIN 83 89 POLY-ARG.
FT DOMAIN 123 137 POLY-GLU.
FT DOMAIN 162 166 POLY-GLY.
FT DOMAIN 434 437 POLY-GLN.
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 643 643 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 600 600 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
SQ SEQUENCE 654 AA: 73473 MW: 8693651A30BD36D4 CRC64:

```

Query Match 75.6%; Score 59; DB 1; Length 654;
 Best Local Similarity 73.3%; Pred. No. 0.015;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 FAEADPTSGFSSIP 15
 |||||:|:| |
 DB 499 FAEADPTTHQOSIP 513

RESULT 6
 C1K4_MUSPF STANDARD: PRT: 654 AA.
 ID C1K4_MUSPF Q28527:
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.4 (FK1).
 GN KCNA4.
 OS Muscula putorius furo (Ferret).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustellidae; Mustela.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART VENTRICLE;
 RX MEDLINE=95029958; PubMed=7943383;
 RA Comer M.B., Campbell D.L., Rasmussen R.L., Lanson D.R.,
 RA Morales M.J., Zhang Y., Strauss H.C.;
 RT "Cloning and characterization of an Ito-like potassium channel from
 RT ferret ventricle."
 RL Am. J. Physiol. 267:H1383-H1395(1994).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. LEFT AND RIGHT
 CC VENTRICLE, AND KIDNEY BUT NOT IN SKELETAL MUSCLE, ENDOTHELIAL
 CC CELLS, AORTA, AND LIVER.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
 CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U06156; AAB60261.1; -
 DR HSSP: P15385; IZRO.
 DR INTERPRO: IPR000636; -
 DR INTERPRO: IPR003091; -
 DR PFM: PF00520; Ion_trans; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KM Glycoprotein; Multigene family; Ion transport; Voltage-gated channel;
 FT TRASMEN 309 327
 FT TRASMEN 372 393
 FT TRASMEN 405 425
 FT TRASMEN 444 462
 FT TRASMEN 479 498
 FT TRASMEN 540 562
 SEGMENT S1 (POTENTIAL).
 SEGMENT S2 (POTENTIAL).
 SEGMENT S3 (POTENTIAL).
 SEGMENT S4 (POTENTIAL).
 SEGMENT S5 (POTENTIAL).
 SEGMENT S6 (POTENTIAL).

Query Match 75.6%; Score 59; DB 1; Length 654;
 Best Local Similarity 73.3%; Pred. No. 0.015;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 FAEADPTSGFSSIP 15
 |||||:|:| |
 DB 499 FAEADPTTHQOSIP 513

RESULT 7
 C1K4_RAT STANDARD: PRT: 655 AA.
 ID C1K4_RAT P15385:
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.4 (RCK4) (RHK1) (RK4).
 GN KCNA4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=90039914; PubMed=2555158;
 RA Stuehmer W., Ruppersberg J.P., Schroeter K.H., Sakmann B.,
 RA Stocker M., Giese K.P., Perschke A., Baumann A., Pongs O.;
 RT "Molecular basis of functional diversity of voltage-gated potassium
 RT channels in mammalian brain."
 RL EMBO J. 8:3235-3244(1989).
 CC [2]
 CC SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=HEART;
 RX MEDLINE=90346174; PubMed=2384173;
 RA Tseng-Crank J., Tseng G.-N., Schwartz A., Tanouye M.A.;
 RT "Molecular cloning and functional expression of a potassium channel
 RT cDNA isolated from a rat cardiac library."
 RL FEBS Lett. 268:63-68(1990).
 CC [3]
 CC STRUCTURE BY NMR OF 1-37.
 RX MEDLINE=97152495; PubMed=9000078;
 RA Antz C., Geyer M., Fakler B., Schott M.K., Guy H.R., Frank R.,
 RA Ruppersberg J.P., Kalbitzer H.R.;
 RT "NMR structure of inactivation gates from mammalian voltage-dependent
 RT potassium channels."
 RL Nature 385:272-275(1997).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: HEART AND BRAIN.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS

CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X16002; CA43133.1; -
CC DR EMBL: M32867; AAA41469.1; -
CC DR PIR: S06710; S06710.
CC DR PDB: 1ZTO; 05-JUN-97.
CC DR INTERPRO: IPR000636; -
CC DR INTERPRO: IPR003091; -
CC DR PFAM: PF00520; Ion_trans; 1.
CC DR PRINTS: PR00169; KCHANNEL.
CC KW Glycoprotein; Multigene family; Ion transport; Voltage-gated channel;
CC Ionic channel; Transmembrane; Phosphorylation; 3D-structure.
CC -----
CC TRANSMEM 310 328 SEGMENT S1 (POTENTIAL).
CC FT TRANSMEM 373 394 SEGMENT S2 (POTENTIAL).
CC FT TRANSMEM 406 426 SEGMENT S3 (POTENTIAL).
CC FT TRANSMEM 445 463 SEGMENT S4 (POTENTIAL).
CC FT TRANSMEM 480 499 SEGMENT S5 (POTENTIAL).
CC FT TRANSMEM 541 563 SEGMENT S6 (POTENTIAL).
CC FT DOMAIN 38 50 POLY-ALA.
CC FT DOMAIN 62 65 POLY-HIS.
CC FT DOMAIN 92 95 POLY-LYS.
CC FT DOMAIN 124 138 POLY-GLU.
CC FT DOMAIN 163 167 POLY-GLY.
CC FT DOMAIN 183 183 POLY-GLN.
CC FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 644 644 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT MOD_RES 601 601 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
CC FT CONFLICT 42 42 A -> L (IN REF. 2).
CC FT CONFLICT 84 88 EEEAT -> RRRRO (IN REF. 2).
CC FT CONFLICT 95 95 MISSING (IN REF. 2).
CC FT CONFLICT 310 310 G -> A (IN REF. 2).
CC SQ SEQUENCE 655 AA; 73390 MW; 40AEF2P901A05E43 CRC64;

Query Match 75.6%; Score 59; DB 1; Length 655;
Best Local Similarity 73.3%; Pred. No. 0.015;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAEDDPTSGFSSIP 15
Db 500 FAEDDPTGFGSIP 514

RESULT 8
CIR4_BOVIN STANDARD; PRT; 660 AA.
ID CIR4_BOVIN
AC 005037;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL4 (BAK4).
GN KCNA4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=ADRENAL MEDULLA;
RX MEDLINE=92371645; PubMed=1505668;
RA Garcia-Guzman M., Calvo S., Cerna V., Criado M.;

RT "Molecular cloning and permanent expression in a neuroblastoma cell
RT line of a fast inactivating potassium channel from bovine adrenal
RT medulla."
RL FEBS Lett. 308:283-289(1992).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROETRAIMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC -----
CC EMBL: X57033; CA40349.1; -
CC DR HSSP: P15385; 1ZTO.
CC DR INTERPRO: IPR000636; -
CC DR INTERPRO: IPR003091; -
CC DR PFAM: PF00520; Ion_trans; 1.
CC DR PRINTS: PR00169; KCHANNEL.
CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Glycoprotein; Multigene family; Phosphorylation.
CC FT TRANSMEM 316 334 SEGMENT S1 (POTENTIAL).
CC FT TRANSMEM 379 400 SEGMENT S2 (POTENTIAL).
CC FT TRANSMEM 412 432 SEGMENT S3 (POTENTIAL).
CC FT TRANSMEM 451 465 SEGMENT S4 (POTENTIAL).
CC FT TRANSMEM 486 505 SEGMENT S5 (POTENTIAL).
CC FT TRANSMEM 547 569 SEGMENT S6 (POTENTIAL).
CC FT DOMAIN 38 50 POLY-ALA.
CC FT DOMAIN 53 59 POLY-GLY.
CC FT DOMAIN 62 65 POLY-HIS.
CC FT DOMAIN 83 87 POLY-ARG.
CC FT DOMAIN 131 137 POLY-GLU.
CC FT DOMAIN 162 173 POLY-GLN.
CC FT CARBOHYD 441 444 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 360 360 PHOSPHORYLATION (BY CAPK)
CC FT MOD_RES 607 607 (BY SIMILARITY).
CC SQ SEQUENCE 660 AA; 73512 MW; A1FAE59677929D5 CRC64;

Query Match 75.6%; Score 59; DB 1; Length 660;
Best Local Similarity 73.3%; Pred. No. 0.015;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAEDDPTSGFSSIP 15
Db 506 FAEDDPTGFGSIP 520

RESULT 9
CIR6_HUMAN STANDARD; PRT; 529 AA.
ID CIR6_HUMAN
AC P17658;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)


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DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL6 (HBR2).
GN      KCNA6.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-BRAIN.
RC      MEDLINE=90269208; PubMed=2347305;
RA      Grupe A., Schroeter K.H., Ruppersberg J.P., Stocker M., Drewes T.,
RA      Becke S., Pongs O.;
RT      "Cloning and expression of a human voltage-gated potassium channel. A
RL      novel member of the RCK potassium channel family.";
EMBL J. 9:11749-11756(1990).
CC      -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC      ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC      CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC      MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC      WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC      GRADIENT.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC      -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC      CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC      EVERY THIRD POSITION.
CC      -1- MISCELLANEOUS: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC      ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC      COMPARTMENTS.
CC      -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC      CLASS, BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X17622; CAA35623.1; -.
DR      PIR; S15057; S15057.
DR      MIM; 176257; -.
DR      INTERPRO; IPR000636; -.
DR      INTERPRO; IPR003091; -.
DR      PFM; PF00520; Ion_trans; 1.
DR      PRINTS; PR00169; KCHANNEL.
KW      Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW      Glycoprotein; Multigene family; Phosphorylation.
FT      TRANSMEM 175 193 SEGMENT S1.
FT      TRANSMEM 263 284 SEGMENT S2.
FT      TRANSMEM 296 316 SEGMENT S3.
FT      TRANSMEM 340 360 SEGMENT S4.
FT      TRANSMEM 376 396 SEGMENT S5.
FT      TRANSMEM 437 457 SEGMENT S6.
FT      MOD_RES 511 511 PHOSPHORYLATION (BY CAPK)
FT      (PROBABLE).
SQ      SEQUENCE 529 AA; 58728 MM; CEF0710A1F9CD69F CRC64;
OY      1 FAEADPTSGFSSP 15
OY      ||||| | | | | |
DB      396 FAEADDDSLPFSIP 410

Query Match      62.8%; Score 49; DB 1; Length 529;
Best Local Similarity 73.3%; Pred. No. 0.63;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 10
ID      C1K5_RAT
AC      P19024; STANDARD; PRT; 602 AA.
DT      01-NOV-1990 (Rel. 16, Created)

```

Query Match 62.8%; Score49; DB 1; Length 602;

Best Local Similarity 73.3%; Pred. No. 0.72;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FAEADPTGFSIP 15
11111: 11111
Db 443 FAEADNHSFSSIP 457

RESULT 11
CIRK1_HUMAN STANDARD; PRT: 495 AA.
ID CIRK1_HUMAN 009470:
AC 009470:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.1 (HVK1).
GN KCVML.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RA Ramaswami M., Gautam M., Kamb A., Rudy B., Tanouye M.A.,
RA Machew M.K.,
RT "Human potassium channel genes: molecular cloning and functional
expression."
RT Mol. Cell. Neurosci. 1:214-223(1990).
RN [2]
RP VARIANTS AEK PHE-174; SER-239; ILE-249 AND ALA-408.
RX MEDLINE-95144169; PubMed-7842011;
RA Browne D.L., Ganchar S.T., Nult J.G., Brunt E.R.P., Smith E.A.,
RA Kramer P., Ilt M.,
RT "Episodic ataxia/myokymia syndrome is associated with point mutations
in the human potassium channel gene, KCVML."
RT Nat. Genet. 8:136-140(1994).
RN [3]
RP VARIANTS AEK ARG-177; ALA-226 AND ILE-404.
RX MEDLINE-98260872; PubMed-9600245.
RA Scheffer H., Brunt E.R.P., Mol G.J.J., van der Vlies P., Stulp R.P.,
RA Verling E., Mantel G., Averbach Y.N., Hofstra R.M.W., Buys C.H.C.M.,
RT "Three novel KCML mutations in episodic ataxia type I families."
RT Hum. Genet. 102:464-466(1998).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
GRADIENT.
CC -1- SUBUNIT: HETEROOTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
EVERY THIRD POSITION.
CC -1- DISEASE: DEFECTS IN KCML ARE THE CAUSE OF MYOKYMIA WITH PERIODIC
ATAXIA (AEK) (PAROXYSMAL OR EPISODIC ATAXIA (EA)). A DISEASE
CHARACTERIZED BY CONTINUOUS MUSCLE MOVEMENT (MYOKYMIA) AND
PERIODIC ATAXIA.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC -----

DR EMBL; L02750; AAA36139.1; -.
DR HSSP; P03621; 21FN.
DR MIM; 176260; -.
DR MIM; 160120; -.
DR INTERPRO; IPR000636; -.
DR INTERPRO; IPR003091; -.
DR PFM; PF00520; Ion_trans, 1.
DR PRINTS; PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation; Disease mutation.
FT TRANSMEM 168 186
FT TRANSMEM 221 242
FT TRANSMEM 254 274
FT TRANSMEM 290 309
FT TRANSMEM 326 345
FT TRANSMEM 387 408
FT CARBOHYD 207 207
FT MOD_RES 322 322
FT MOD_RES 445 445
FT MOD_RES 174 174
FT VARIANT 177 177
FT VARIANT 226 226
FT VARIANT 239 239
FT VARIANT 249 249
FT VARIANT 404 404
FT VARIANT 408 408
FT SEQUENCE 495 AA; 56541 MW; 0A1B1AB0536F5CBA CRG64;

Query Match 61.5%; Score 48; DB 1; Length 495;
Best Local Similarity 66.7%; Pred. No. 0.87;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 FAEADPTGFSIP 15
11111: 11111
Db 346 FAEAEASHFSSIP 360

RESULT 12
CIRK1_MOUSE STANDARD; PRT: 495 AA.
ID CIRK1_MOUSE P16388:
AC P16388:
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.1 (MK1).
GN KCVML.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90161996; PubMed-2305265;
RA Chandry K.G., Williams C.B., Spencer R.H., Aguilar B.A.,
RA Ganshans S., Tempel B.L., Gutman G.A.,
RT "A family of three mouse potassium channel genes with intronless
coding regions."
RT Science 247:973-975(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RX MEDLINE-88189348; PubMed-2451788;
RA Tempel B.L., Jan Y.N., Jan L.Y.,
RT "Cloning of a probable potassium channel gene from mouse brain.";

```

RL Nature 332:837-839(1988).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROPTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC -----
DR EMBL: M30439; AAA39711.1; -
DR EMBL: Y00305; CAA68408.1; -
DR PIR: S06378; S06378.
DR PIR: A40090; A40090.
DR HSSP: P03621; 2IFN.
DR MGD: M61:96654; KCNA1.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR003091; -.
DR PIR: PF00520; Ion.trans. 1.
DR PRINTS: PR00169; KCHANNEL.
DR KMW: Glycophorin; Transmembrane; Ion transport; Voltage-gated channel;
DR KMW: Glycophorin; Multigene family; Phosphorylation.
FT TRANSMEM 168 186 SEGMENT S1.
FT TRANSMEM 221 242 SEGMENT S2.
FT TRANSMEM 254 274 SEGMENT S3.
FT TRANSMEM 290 309 SEGMENT S4.
FT TRANSMEM 326 345 SEGMENT S5.
FT TRANSMEM 367 408 SEGMENT S6.
FT CAROHD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 322 322 PHOSPHORYLATION (BY CAPK)
FT FT PHOSPHORYLATION.
FT MOD_RES 446 446 PHOSPHORYLATION (BY CAPK)
FT FT (POTENTIAL).
SQ SEQUENCE 495 AA; 56409 MW; C9249F130E943D3D CRC64;

Query Match 61.5%; Score 48; DB 1; Length 495;
Best Local Similarity 66.7%; Pred. No. 0.87;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAEADPTSGFSSIP 15
DB 346 FAEAEAEHSSIP 360

RESULT 13
CIR1_RAT
ID CIR1_RAT STANDARD: PRT; 495 AA.
AC P10499;
DT 01-APR-1990 (rel. 14, Created)
DT 01-APR-1990 (rel. 14, Last sequence update)
DT 15-JUL-1998 (rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (1A) (RBK1) (RCK1).
GN KCNA1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=89052659; PubMed=3191911;
RA Baumann A., Grupe A., Ackermann A., Pongs O.;
RT "Structure of the voltage-dependent potassium channel is highly
RT conserved from Drosophila to vertebrate central nervous systems.";
RL EMBL J. 7:2457-2463(1988).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=89203264; PubMed=2539643;
RA Christie M.J., Adelman J.P., Douglass J., North R.A.;
RT "Expression of a cloned rat brain potassium channel in Xenopus
RT oocytes.";
RL Science 244:221-224(1989).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROPTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X12589; CAA31102.1; -
DR EMBL: M26161; AAA1982.1; -
DR PIR: A41353; A41353.
DR PIR: S01161; S01161.
DR HSSP: P03621; 2IFN.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR003091; -.
DR PIR: PF00520; Ion.trans. 1.
DR PRINTS: PR00169; KCHANNEL.
DR KMW: Glycophorin; Transmembrane; Ion transport; Voltage-gated channel;
DR KMW: Glycophorin; Multigene family; Phosphorylation.
FT TRANSMEM 168 186 SEGMENT S1.
FT TRANSMEM 221 242 SEGMENT S2.
FT TRANSMEM 254 274 SEGMENT S3.
FT TRANSMEM 290 309 SEGMENT S4.
FT TRANSMEM 326 345 SEGMENT S5.
FT TRANSMEM 367 408 SEGMENT S6.
FT CAROHD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 322 322 PHOSPHORYLATION (BY CAPK)
FT FT PHOSPHORYLATION.
FT MOD_RES 445 445 PHOSPHORYLATION (BY CAPK)
FT FT (POTENTIAL).
SQ SEQUENCE 495 AA; 56379 MW; 29804463133F5D31 CRC64;

Query Match 61.5%; Score 48; DB 1; Length 495;
Best Local Similarity 66.7%; Pred. No. 0.87;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAEADPTSGFSSIP 15

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Db 346 FAEAEASHPSIP 360

RESULT 14
CIRK6_RAT
ID CIRK6_RAT STANDARD: PRT: 530 AA.
AC P17659; P19025;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.6 (RCK2) (KV2).
GN KCNA6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN CORTEX;
RX MEDLINE=90269208; Pubmed=2347305;
RA Grupe A., Schroeter K.H., Ruppersberg J.P., Stocker M., Drewes T.,
RA Beckh S., Pongs O.;
RT "Cloning and expression of a human voltage-gated potassium channel. A
RT novel member of the RCK potassium channel family.";
RL EMBL J. 9:1749-1756(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=90297965; Pubmed=1993474;
RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B.,
RA Folander K., Luneau C.J., Antanavage J., Oliva C., Buhrow S.A.,
RA Bennett C., Stein R.B., Kaczmarek L.M.;
RT "Electrophysiological characterization of a new member of the RCK
RT family of rat brain K+ channels.";
RL FEBS Lett. 278:55-60(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91130598; Pubmed=1993474;
RA Kirsch G.E., Drewe J.A., Verma S., Brown A.M., Joho R.H.;
RT "Electrophysiological characterization of a new member of the RCK
RT family of rat brain K+ channels.";
RL FEBS Lett. 278:55-60(1991).
RN [4]
RP FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
RP ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
RP CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
RP MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
RP WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
RP GRADIENT.
RP SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
RN [5]
RP TISSUE SPECIFICITY: BRAIN.
RN [6]
RP DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
RP CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
RP EVERY THIRD POSITION.
RN [7]
RP MISCELLANEOUS: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
RP ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
RP COMPARTMENTS.
RN [8]
RP CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
RN [9]
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DR EMBL: X17621; CA35622.1; -
DR EMBL: M21159; AAA41499.1; ALT_SEQ.
DR PIR: JH0167; JH0167.
DR PIR: S12786; S12786.
DR INTERPRO: IPR000636; -

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DR INTERPRO: IPR003091; -
DR PFAM: PF00520; Ion_trans; 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 175 193 SEGMENT S1.
FT TRANSMEM 264 285 SEGMENT S2.
FT TRANSMEM 297 317 SEGMENT S3.
FT TRANSMEM 341 361 SEGMENT S4.
FT TRANSMEM 377 397 SEGMENT S5.
FT TRANSMEM 438 458 SEGMENT S6.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 222 222 PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT MOD_RES 512 512 PHOSPHORYLATION (BY CAK) (PROBABLE).
FT MOD_RES 528 528 PHOSPHORYLATION (BY CAK) (POTENTIAL).
FT CONFLICT 241 241 S -> L (IN REF. 3).
FT CONFLICT 333 333 R -> G (IN REF. 2).
SQ SEQUENCE 530 AA; 58883 MW; 30A9774B66CF1DA5 CRC64;

Query Match 61.58; Score 48; DB 1; Length 530;
Best Local Similarity 73.38; Pred. No. 0.93;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 397 FAEADVDLSRPSIP 411

RESULT 15
CIRK5_MUSPF
ID CIRK5_MUSPF STANDARD: PRT: 601 AA.
AC P79197;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5.
GN KCNA5.
OS Mus musculus (Mus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART ATRIUM;
RA Schwiegel T., Folander K., Swanson R.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
RP ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
RP CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
RP MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
RP WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
RP GRADIENT (BY SIMILARITY).
RN [3]
RP SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
RN [4]
RP DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
RP CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
RP EVERY THIRD POSITION.
RN [5]
RP DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
RP RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
RP IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
RP TO SPECIFIC SUBCELLULAR COMPARTMENTS.
RN [6]
RP SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
RP CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
RN [7]
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DR EMBL: U45979; AAB41145.1; -
 DR INTERPRO: IPR000636; -
 DR INTERPRO: IPR003091; -
 DR PFW: PF00520; Ion_Trans; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 240 258 SEGMENT S1.
 FT TRANSMEM 314 334 SEGMENT S2.
 FT TRANSMEM 345 366 SEGMENT S3.
 FT TRANSMEM 386 407 SEGMENT S4.
 FT TRANSMEM 422 443 SEGMENT S5.
 FT TRANSMEM 483 504 SEGMENT S6.
 FT DOMAIN 370 375 POLY-GLY.
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 601 AA; 65889 MW; 142DB9F8CBB43FE0 CRC64;

Query Match 61.5%; Score 48; DB 1; Length 601;
 Best Local Similarity 66.7%; Pred. No. 1.1;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAADDPTSGESSIP 15
 |||||: . |||||
 Db 442 FAADNQTTHSSIP 456

Search completed: February 2, 2001, 10:41:51
 Job time: 315 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 2, 2001, 10:39:12 ; Search time 62.83 Seconds
(without alignments)
27.982 Million cell updates/sec

Title: US-09-273-217-4
Perfect score: 78
Sequence: 1 FAADDPSTGFSIP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	516	6 Q28656	Q28656 oryctolagus
2	74	94.9	27	13 Q73609	Q73609 gallus gall
3	73	93.6	136	6 Q09077	Q09077 sus scrofa
4	72	92.3	483	13 Q91829	Q91829 oncorhynch
5	72	91.8	27	13 Q73608	Q73608 gallus gall
6	56	71.8	494	13 Q91830	Q91830 oncorhynch
7	56	71.8	511	4 Q16322	Q16322 homo sapien
8	56	71.8	725	6 Q28649	Q28649 oryctolagus
9	54	69.2	662	13 Q9YXG8	Q9YXG8 gallus gall
10	50	64.1	602	11 Q921R6	Q921R6 mus musculu
11	48.5	62.2	543	10 Q9SBA8	Q9SBA8 arabidopsis
12	48	61.5	529	11 Q619Z3	Q619Z3 mus musculu
13	48	61.5	593	6 Q28248	Q28248 canis famli
14	47	60.3	512	5 Q28597	Q28597 schistosoma
15	47	60.3	552	10 Q24019	Q24019 lycopersico
16	46	59.0	123	6 Q9NOE4	Q9NOE4 sus scrofa
17	46	59.0	141	6 Q09074	Q09074 sus scrofa
18	46	59.0	141	6 Q09075	Q09075 sus scrofa
19	46	59.0	460	5 Q09658	Q09658 caenorhabdi

20	46	59.0	476	6 Q08635	Q08635 bos taurus
21	46	59.0	490	5 Q9XXD1	Q9XXD1 caenorhabdi
22	46	59.0	499	6 Q28293	Q28293 canis famli
23	46	59.0	499	6 Q9MYX3	Q9MYX3 oryctolagus
24	45	57.7	273	6 Q9XSP9	Q9XSP9 oryctolagus
25	45	57.7	433	10 Q9SUY9	Q9SUY9 arabidopsis
26	45	57.7	489	13 Q91781	Q91781 xenopus lae
27	45	57.7	905	5 Q26344	Q26344 aplysia sp.
28	44	56.4	330	2 Q9K987	Q9K987 bacillus ha
29	43	55.1	2016	5 Q9VL57	Q9VL57 drosophila
30	42	53.8	898	13 Q91592	Q91592 xenopus lae
31	42	53.8	908	5 Q18476	Q18476 loligo peal
32	42	53.8	998	6 Q9N1D1	Q9N1D1 gorilla gor
33	42	53.8	1104	3 Q9P553	Q9P553 neotrospora
34	41	52.6	41	4 Q9UD04	Q9UD04 homo sapien
35	41	52.6	206	2 Q910X8	Q910X8 streptomyc
36	41	52.6	238	10 Q39962	Q39962 hevea bras
37	41	52.6	422	5 Q9VEX2	Q9VEX2 drosophila
38	41	52.6	488	5 Q25376	Q25376 loligo opal
39	41	52.6	515	5 Q16968	Q16968 aplysia cal
40	41	52.6	575	12 Q65530	Q65530 bovine herp
41	41	52.6	575	12 Q39506	Q39506 bovine herp
42	41	52.6	575	12 Q9JE43	Q9JE43 bovine herp
43	41	52.6	597	6 Q9FS07	Q9FS07 bos taurus
44	41	52.6	834	2 Q914D0	Q914D0 streptococ
45	41	52.6	2134	12 Q9YLS4	Q9YLS4 avian encep

ALIGNMENTS

RESULT	1				
Q28656	ID	Q28656	PRELIMINARY:	PRT:	516 AA.
AC	Q28656				
DT	01-NOV-1996	(TREMBLrel. 01, Created)			
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)			
DT	01-OCT-2000	(TREMBLrel. 15, Last annotation update)			
DE	GLIBENCLAMIDE-SENSITIVE VOLTAGE-GATED POTASSIUM CHANNEL.				
GN	KVL3-GLYB.				
OS	Oryctolagus cuniculus (Rabbit).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX	NCBI_TaxID=9986;				
RM	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-NEW ZEALAND WHITE;				
RX	MEDLINE=96249424; PubMed=8647945;				
RA	Yao X., Chang A.Y., Boulpaep E.L., Segal A.S., Desir G.V.;				
RT	Molecular cloning of a glibenclamide-sensitive, voltage-gated				
RT	potassium channel expressed in rabbit kidney."				
RL	J. Clin. Invest. 97:2525-2533(1996).				
DR	EMBL:	U38240;	AKC24718.1;		
DR	HSSP:	054397;	1BU8.		
DR	INTERPRO:	IPR000636;	-;		
DR	INTERPRO:	IPR001622;	-;		
DR	INTERPRO:	IPR003091;	-;		
DR	INTERPRO:	IPR003131;	-;		
DR	PFAM:	PF00520;	Ion_trans. 1.		
DR	PFAM:	PF02214;	K_tetra. 1.		
DR	PRINTS:	PRO0169;	KCHANNEL.		
KW	Ionic channel.				
SQ	SEQUENCE 516 AA; 57430 MW; 795E8498BCA7CAA CRC64;				
Query Match		100.0%;	Score 78;	DB 6;	Length 516;
Best Local Similarity		100.0%;	Pred. NO. 8.8e-06;		
Matches 15;	Conservative	0;	Mismatches	0;	Indels 0;
Gaps					
Oy	1	FAADDPSTGFSIP 15			
Db	359	FAADDPSTGFSIP 373			

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RESULT 2
ID 073609 PRELIMINARY; PRT: 27 AA.
AC 073609:
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE SHAKER-LIKE VOLTAGE-GATED POTASSIUM CHANNEL CKV1.1 (FRAGMENT).
GN CKV1.1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=COCHLEAR DUCT;
RX MEDLINE=98141813; PubMed=9473273;
RA Peale F.V., Mason K., Hunter A.W., Bothwell M.;
RT "Multiplex display polymerase chain reaction amplifies and resolves
RT related sequences sharing a single moderately conserved domain.";
RL Anal. Biochem. 256:158-168(1998).
DR EMBL: U62142; AAC06194.1; -.
KW Ionic channel.
FT NON_TER 1
FT TER 27
SQ SEQUENCE 27 AA; 2936 MW; 06BEFB440D5D9DD5 CRC64;

Query Match
Best Local Similarity 94.9%; Score 74; DB 13; Length 27;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAADDPGSGSSIP 15
Db 4 FAADDPGSGSSIP 18

RESULT 3
ID 009077 PRELIMINARY; PRT: 136 AA.
AC 009077:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE POTASSIUM CHANNEL PROTEIN (CLONE LLC3) (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92125505; PubMed=1733291;
RA Desit G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,
RA Igarashi P.;
RT "Isolation of putative voltage-gated epithelial K-channel isoforms
RT from rabbit kidney and LLC-PK1 cells.";
RL Am. J. Physiol. 262:151-157(1992).
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN RENAL EPITHELIAL TRANSPORT
CC AND MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF
CC MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO
CC THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A
CC POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN
CC ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
CC IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: BELONGS TO THE SHAKER-RELATED POTASSIUM CHANNEL
CC SUBFAMILY 1.
DR HSSP: Q54397; 1BL8.
DR INTERPRO: IPR000636; -.

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DR INTERPRO: IPR003091; -.
DR PFAM: PF00520; Ion_trans. 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family.
FT NON_TER 1
FT TRANSMEM 1
FT TRANSMEM <1 6 SEGMENT S3.
FT TRANSMEM 22 39 SEGMENT S4.
FT TRANSMEM 56 75 SEGMENT S5.
FT TRANSMEM 116 136 SEGMENT S6.
FT NON_TER 136
SQ SEQUENCE 136 AA; 14827 MW; E8D95E192AA7FB97 CRC64;

Query Match
Best Local Similarity 93.3%; Score 73; DB 6; Length 136;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FAADDPGSGSSIP 15
Db 76 FREADDPGSGSSIP 90

RESULT 4
ID 091829 PRELIMINARY; PRT: 483 AA.
AC 091829:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE SHAKER-RELATED POTASSIUM CHANNEL TSHAZ.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RX MEDLINE=98146169; PubMed=9486764;
RA Nguyen T.D., Jeserich G.;
RT "Molecular structure and expression of shaker type potassium channels
RT in gill cells of trout CNS.";
RL J. Neurosci. Res. 51:284-292(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RA Nguyen T.D., Jeserich G.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF252302; AAF70088.1; -.
KW Ionic channel.
SQ SEQUENCE 483 AA; 54955 MW; 68A78A8ECAA424956 CRC64;

Query Match
Best Local Similarity 92.3%; Score 72; DB 13; Length 483;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FAADDPGSGSSIP 15
Db 345 FAADDPGSGSSIP 359

RESULT 5
ID 073608 PRELIMINARY; PRT: 27 AA.
AC 073608:
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE SHAKER-LIKE VOLTAGE-GATED POTASSIUM CHANNEL CKV1.2 (FRAGMENT).
GN CKV1.2.
OS Gallus gallus (Chicken).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archaeosuria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LECHORN; TISSUE-COCHLEAR DUCT;
RX MEDLINE=98141813; PubMed=9473273;
RA Peale F.V., Mason K., Hunter A.W., Bothwell M.;
RT "Multiplex display polymerase chain reaction amplifies and resolves
RT related sequences sharing a single moderately conserved domain.";
RL Anal. Biochem. 256:158-168(1998).
DR EMBL: U62141; AAC06193.1; -.
KW Ionic channel.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 3085 MW; EB081A9F65EAC123 CRC64;

Query Match 71.8%; Score 56; DB 13; Length 27;
Best Local Similarity 73.3%; Pred. No. 0.003;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAADDPTSGFSSIP 15
   |||:|:| |||||
Db 4 FAEVDEPQSHFSSIP 18

RESULT 6
C91830
AC 091830. PRELIMINARY; PRT; 494 AA.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE SHAKE-RELATED POTASSIUM CHANNEL TSHAL.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=98146169; PubMed=9486764;
RA Nguyen T.D., Jeserich G.;
RT "Molecular structure and expression of shaker type potassium channels
RT in glial cells of trout CNS.";
RL J. Neurosci. Res. 51:284-292(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Nguyen T.D., Jeserich G.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF252301; AAF70087.1; -.
KW Ionic channel.
SQ SEQUENCE 494 AA; 55899 MW; AF66998F97F22CD4 CRC64;

Query Match 71.8%; Score 56; DB 13; Length 494;
Best Local Similarity 73.3%; Pred. No. 0.071;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAADDPTSGFSSIP 15
   |||:|:| |||||
Db 343 FAEADPEQSFESIP 357

RESULT 7
C916322
AC 016322. PRELIMINARY; PRT; 511 AA.
DT 01-NOV-1996 (TREMBLrel. 01, Created)

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DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CYCLIC GMP GATED POTASSIUM CHANNEL.
GN KCNI OR C2-3A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97321042; PubMed=9177773;
RA Orlas M., Bray-Ward P., Curran M.E., Keating M.T., Desir G.V.;
RT "Genomic localization of the human gene for KCNA10, a cGMP-activated K
RT channel.";
RL Genomics 42:33-37(1997).
RN [2]
RP SEQUENCE OF 434-479 FROM N.A.
RX MEDLINE=95309039; PubMed=7789190;
RA Landes G.M., Curran M.E., Keating M.T.;
RT "Molecular characterization and refined genomic localization of three
RT human potassium ion channel genes.";
RL Cytogenet. Cell Genet. 70:280-284(1995).
DR EMBL: U96110; AAC51333.1; -.
DR EMBL: S77547; AAB34663.1; -.
DR HSSP: Q54397; IBL8.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR001622; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFAM: PF00520; Ion_trans; 1.
DR PFAM: PF02214; K_tetra; 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel.
SQ SEQUENCE 511 AA; 57784 MW; 1B0981CD68745F29 CRC64;

Query Match 71.8%; Score 56; DB 4; Length 511;
Best Local Similarity 73.3%; Pred. No. 0.074;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAADDPTSGFSSIP 15
   |||:|:| |||||
Db 395 FAEVDEPQSHFSSIP 409

RESULT 8
C028649
AC 028649. PRELIMINARY; PRT; 725 AA.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CGMP-GATED POTASSIUM CHANNEL.
GN KCNI.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NEW ZEALAND WHITE;
RX MEDLINE=96102184; PubMed=8524834;
RA Yao X., Segal A.S., Welling P., Zhang X., McNicholas C.M., Engel D.,
RA Boupaep E.L., Desir G.V.;
RT "Primary structure and functional expression of a cGMP-gated potassium
RT channel.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:11711-11715(1995).
DR EMBL: U38182; AAB92054.1; -.
DR HSSP: Q54397; IBL8.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR001622; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.

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DR PF00520; Ion.trans; 1.
 DR PF02214; K.tetra; 1.
 DR PRINTS; PR00169; KCHANNEL.
 KM Ionic channel.
 SQ SEQUENCE 725 AA; 80964 MW; 09C538F7BF4EDBD CRC64;

Query Match 71.88; Score 56; DB 6; Length 725;
 Best Local Similarity 73.38; Pred. No. 0.11;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 FAEADPTSGFSSIP 15
 |||||:|||||
 Db 609 FAEVDEPESHSSIP 623

RESULT 9
 O9YX8 PRELIMINARY; PRT: 662 AA.
 AC O9YX8;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE POTASSIUM CHANNEL SHAKER CKV1.4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxId=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-9197209; PubMed-10095080;
 RA Rajeevan M.S., Hu S., Sakai Y., Sokolowski B.H.A.;
 RT "Cloning and expression of Shaker alpha- and beta-subunits during
 RT inner ear development."
 RL Brain Res. Mol. Brain Res. 66:83-93(1999).
 DR EMBL: U02365; AAD11454.1; -.
 DR HSSP: P13385; 1270.
 DR INTERPRO: IPR000636; -.
 DR INTERPRO: IPR001622; -.
 DR INTERPRO: IPR003091; -.
 DR INTERPRO: IPR003131; -.
 DR PFAM: PF00520; Ion.trans; 1.
 DR PFAM: PF02214; K.tetra; 1.
 DR PRINTS; PR00169; KCHANNEL.
 KM Ionic channel.
 SQ SEQUENCE 662 AA; 74061 MW; 7DB994240DF58007 CRC64;

Query Match 69.28; Score 54; DB 13; Length 662;
 Best Local Similarity 66.78; Pred. No. 0.22;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 OY 1 FAEADPTSGFSSIP 15
 |||||:|||||
 Db 507 FAEADPTSGFSSIP 521

RESULT 10
 O9ZIR6 PRELIMINARY; PRT: 602 AA.
 AC O9ZIR6;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE VENTRICULAR POTASSIUM CHANNEL KV1.5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tanaka H., Janzen K., Winkfein R.J., Fiset C., Clark B., Giles W.R.;

RT "Cloning and functional expression of mouse heart K+ channel alpha-
 RT subunits, Kv1.5, Kv4.2, and Kv4.3."
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF108659; AAD13779.1; -.
 DR HSSP: Q54397; 1BL8.
 DR INTERPRO: IPR000636; -.
 DR INTERPRO: IPR001622; -.
 DR INTERPRO: IPR003091; -.
 DR INTERPRO: IPR003131; -.
 DR PFAM: PF00520; Ion.trans; 1.
 DR PFAM: PF02214; K.tetra; 1.
 DR PRINTS; PR00169; KCHANNEL.
 KM Ionic channel.
 SQ SEQUENCE 602 AA; 66579 MW; 02926E85DC022DDA CRC64;

Query Match 64.18; Score 50; DB 11; Length 602;
 Best Local Similarity 73.38; Pred. No. 1;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 FAEADPTSGFSSIP 15
 |||||:|||||
 Db 443 FAEADNGSHSSIP 457

RESULT 11
 O9SBA8 PRELIMINARY; PRT: 543 AA.
 ID O9SBA8;
 AC O9SBA8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE GTP CYCLOHYDROLASE II / 3,4-DIHYDROXY-2-BUTANONE-4-PHOSPHATE SYNTHASE.
 GN RIBA.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Herz S.W., Eberhardt S., Bacher A.;
 RT "Biosynthesis of riboflavin in plants. The riba gene of Arabidopsis
 RT thaliana specifies a bifunctional GTP cyclohydrolase II / 3,4-
 RT dihydroxy-2butanone-4-phosphate synthase."
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A1000053; CA03884.1; -.
 DR INTERPRO: IPR000422; -.
 DR INTERPRO: IPR000926; -.
 DR PFAM: PF00925; GTP_cyclohydrol2; 1.
 DR PFAM: PF00926; DHBP_synthase; 1.
 KM Hydrolase.
 SQ SEQUENCE 543 AA; 59055 MW; 31D89A500E42BF81 CRC64;

Query Match 62.28; Score 48.5; DB 10; Length 543;
 Best Local Similarity 63.28; Pred. No. 1.7;
 Matches 12; Conservative 0; Mismatches 2; Indels 5; Gaps 1;
 OY 2 AEADD-----PTSGFSSIP 15
 |||||:|||||
 Db 114 AEADDPELDLPPTGSSIP 132

RESULT 12
 ID O61923 PRELIMINARY; PRT: 529 AA.
 AC O61923;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE MORINE POTASSIUM CHANNEL PROTEIN.
 GN MK1.6.

```
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mignon M.B., Street V.A., Demas V.P., Tempel B.L.;
RL Epilepsy Res. 0:0-0(0);
DR EMBL: M96688; AAA39772.1; -.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR001622; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFAM: PF00520; ion_trans. 1.
DR PFAM: PF02214; K_tetra. 1.
DR PRINTS: PR00169; KCHANNEL.
KM Ionic channel.
SQ SEQUENCE 529 AA; 58673 MW; 336D78C069ABEADD CRC64;

Query Match
Best Local Similarity 61.5%; Score 48; DB 11; Length 529;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 FAADDPGSGSSIP 15
DB 396 FAADDPVDSLPSIP 410

RESULT 13
O28248 PRELIMINARY; PRT; 593 AA.
AC O28248.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE DELAYED RECTIFIER K+ CHANNEL (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON.
RA Overlurf K.E., Russell S.N., Carl A., Vogalis R., Hart P.J.,
RA Hume J.R., Sanders K.M., Horowitz B.;
RL Am. J. Physiol. 267:0-0(1994).
DR EMBL: U08596; AAA57320.1; -.
DR HSSP: 054397; 1BL8.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR001622; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFAM: PF00520; ion_trans. 1.
DR PFAM: PF02214; K_tetra. 1.
DR PRINTS: PR00169; KCHANNEL.
KM Ionic channel.
FT NON_TER 593
SQ SEQUENCE 593 AA; 65617 MW; 05627873140B228 CRC64;

Query Match
Best Local Similarity 61.5%; Score 48; DB 6; Length 593;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAADDPGSGSSIP 15
DB 435 FAADDPGTHFSSIP 449

RESULT 14
O26597 PRELIMINARY; PRT; 512 AA.
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AC 026597;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE POTASSIUM CHANNEL PROTEIN.
GN SKV1.1.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Neodermata; Trematoda; Digenea;
OC Strigeidae; Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95191947; PubMed=7533899;
RA Kim E., Day T.A., Bennett J.L., Pax R.A.;
RT "Cloning and functional expression of a Shaker-related voltage-gated
RT potassium channel gene from Schistosoma mansoni (Trematoda:
RT Digenea)."
RT Parasitology 110:171-180(1995).
RL EMBL: L26968; AAC37227.1; -.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR001622; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFAM: PF00520; ion_trans. 1.
DR PFAM: PF02214; K_tetra. 1.
DR PRINTS: PR00169; KCHANNEL.
KM Ionic channel; Transmembrane.
SQ SEQUENCE 512 AA; 58602 MW; 265DB2BA31742D39 CRC64;

Query Match
Best Local Similarity 60.3%; Score 47; DB 5; Length 512;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 FAADDPGSGSSIP 15
DB 361 FAADADTSLFRSIP 375

RESULT 15
O24019 PRELIMINARY; PRT; 552 AA.
AC O24019.
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE GTP CYCLOHYDROLASE II/ 3,4-DIHYDROXY-2-BUTANONE-4-PHOSPHATE SYNTHASE.
GN RIBA.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UC82B;
RA Herz S.W., Eberhardt S., Bacher A.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ002298; CAA05308.1; -.
DR INTERPRO: IPR000422; -.
DR INTERPRO: IPR000926; -.
DR PFAM: PF00925; GTP_cyclohydro2. 1.
DR PFAM: PF00926; DHP_synthase. 1.
DR PRODOM: PD003034; -. 1.
KM Hydrolase.
SQ SEQUENCE 552 AA; 59750 MW; C14686752533325D CRC64;

Query Match
Best Local Similarity 60.3%; Score 47; DB 10; Length 552;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 EADDPGSGSSIP 15
```

Fri Feb 2 15:15:43 2001

us-09-273-217-4.rspt

Page 6

Db : | | | | | | | | | |
120 DLRPEGFSSVP 132

Search completed: February 2, 2001, 10:39:13
Job time: 202 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:37:13 ; Search time 38.22 Seconds

(without alignments)
26.649 Million cell updates/sec

Title: US-09-273-217-4

Perfect score: 78

Sequence: 1 FAEDDPTSGFSSIP 15

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR66:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	523	2 A38101	potassium channel
2	78	100.0	523	2 I52990	voltage-gated pota
3	71	91.0	57	2 S09044	potassium channel
4	71	91.0	525	2 A43531	potassium channel
5	71	91.0	528	2 I84205	potassium channel
6	63	80.8	57	2 S09045	potassium channel
7	59	75.6	653	2 A39922	potassium channel
8	59	75.6	654	2 S11049	potassium channel
9	59	75.6	654	2 E39113	potassium channel
10	59	75.6	660	2 S24125	potassium channel
11	50	64.1	49	2 S09049	potassium channel
12	49	62.8	529	2 S12787	potassium channel
13	49	62.8	602	2 JH0166	potassium voltage-
14	48	61.5	57	2 S09042	potassium channel
15	48	61.5	57	2 S09043	potassium channel
16	48	61.5	495	2 I57680	potassium channel
17	48	61.5	495	2 A40090	potassium channel
18	48	61.5	495	2 B39113	potassium channel
19	48	61.5	530	2 JH0167	potassium channel
20	47	60.3	552	2 T06410	GTP cyclohydrolase
21	47	60.3	598	2 S66659	potassium channel
22	47	60.3	613	2 A56031	potassium channel
23	46	59.0	57	2 S09046	potassium channel
24	46	59.0	460	2 T27759	hypothetical prote
25	46	59.0	476	2 S21144	potassium channel
26	46	59.0	490	2 T26983	hypothetical prote
27	46	59.0	499	2 JH0313	potassium channel
28	46	59.0	499	2 I77466	potassium channel
29	46	59.0	499	2 A48672	delayed rectifier

30	46	59.0	499	2 I84204	potassium channel
31	46	59.0	489	2 A33814	potassium channel
32	45	57.7	489	2 I51532	potassium channel
33	44	56.4	514	2 C49507	potassium channel
34	44	56.4	602	2 A49507	potassium channel
35	43	55.1	597	2 A33668	sterol esterase (E
36	42	53.8	334	1 DGBEX2	uracil-DNA glycosy
37	42	53.8	802	2 JH0595	potassium channel
38	42	53.8	1104	2 T49647	MSPI related prote
39	41	52.6	78	2 S12513	delta-conotoxin Tx
40	41	52.6	238	2 T10760	citrate-binding pr
41	41	52.6	414	2 B56711	casein kinase I (E
42	41	52.6	575	2 S35786	glycoprotein 9E -
43	41	52.6	597	2 S51212	Bak5 protein - bov
44	40	51.3	330	2 C69593	3-methyl-2-oxobuta
45	40	51.3	357	2 T09261	JUN kinase-activat

ALIGNMENTS

```

RESULT 1
A38101
potassium channel KCNA3 - human
N:Alternate names: potassium channel HUK3; potassium channel PCN3; shaker-related pot
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 05-Nov-1999
C:Accession: A38101; B38556
J:Altali, B.; Romey, G.; Honore, E.; Schmid-Alliana, A.; Mattei, M.G.; Lesage, F.; Ri
J Biol. Chem. 267, 8650-8657, 1992
A:Title: Cloning, functional expression, and regulation of two K(+) channels in human
A:Reference number: A38101; MUID:92235098
A:Accession: A38101
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-523 <ATT>
A:Cross-references: GB:M65217; NID:g186664; PIDN:AAA59457.1; PID:g186665
R:Philpson, L.H.; Hice, R.E.; Schaefer, K.; Lakendola, J.; Bell, G.I.; Nelson, D.J.;
Proc. Natl. Acad. Sci. U.S.A. 88, 53-57, 1991
A:Title: Sequence and functional expression in Xenopus oocytes of a human insulinoma
A:Reference number: A38556; MUID:91095456
A:Accession: B38556
A:Molecule type: DNA
A:Residues: 1-19, 'G', 21-36, 'V', 38-60, 'L', 62-90, 'V', 92-337, 'S', 339-418, 'S', 420-457, 'LS
A:Cross-references: GB:M55515
A:Gene: GDB: KCNA3
A:Cross-references: GDB:J28079; OMIM:176263
A:Map position: 1p21-p13.3
C:Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; v

Query Match 100.0%; Score 78; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 5,7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAEDDPTSGFSSIP 15
Db 366 FAEDDPTSGFSSIP 380

RESULT 2
I52990
voltage-gated potassium channel - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I52990
R:Gail, Y.C.; Osborne, P.B.; North, R.A.; Dooley, D.C.; Douglass, J.
DNA Cell Biol. 11, 163-172, 1992
A:Title: Characterization and functional expression of genomic DNA encoding the human
A:Reference number: I52990; MUID:92189730
A:Accession: I52990
A:Status: preliminary; translated from GB/EMBL/DBD

```

A:Molecule type: DNA
 A:Residues: 1-523 <RMS>
 A:Cross-references: GB:M38217; NID:g186670; PIDN:AA88073.1; PID:g186671
 C:Genetics:
 A:Gene: HGK5

Query Match 100.0%; Score 78; DB 2; Length 523;
 Best Local Similarity 100.0%; Pred. No. 5,7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FAEADDPPTSGFSSIP 15
 |||||||

Db 366 FAEADDPPTSGFSSIP 380

RESULT 3
 S09044
 potassium channel protein MK-3 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
 C:Accession: S09044
 R:Betsholtz, C.; Baumann, A.; Kenna, S.; Ashcroft, F.M.; Ashcroft, S.J.H.; Berggren, P.C.
 FEBS Lett. 263, 121-126, 1990
 A:Title: Expression of voltage-gated K⁺ channels in insulin-producing cells. Analysis by
 A:Reference number: S09042; MUID:90235950
 A:Accession: S09044
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-57 <BET>

Query Match 91.0%; Score 71; DB 2; Length 57;
 Best Local Similarity 86.7%; Pred. No. 7,4e-06;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 FAEADDPPTSGFSSIP 15
 |||||||

Db 11 FAEADDPSSGFNSIP 25

RESULT 4
 A43531
 potassium channel Kv1.3 - rat
 N:Alternate names: potassium channel Kv3; potassium channel RCK3; potassium channel RCK5
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 05-Nov-1999
 C:Accession: A43531; JH0168; S06708
 R:Douglas, J.; Osborne, P.B.; Cal, Y.C.; Wilkinson, M.; Christie, M.J.; Adelman, J.P.
 J. Immunol. 144, 4841-4850, 1990
 A:Title: Characterization and functional expression of a rat genomic DNA clone encoding
 A:Reference number: A43531; MUID:90278098
 A:Accession: A43531
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-525 <DOU>
 R:Swanson, R.; Marshall, J.; Smith, J.S.; Williams, J.B.; Boyle, M.B.; Folander, K.; Lunt
 Neuron 4, 929-939, 1990
 A:Title: Cloning and expression of cDNA and genomic clones encoding three delayed rectifi
 A:Reference number: JH0166; MUID:90297965
 A:Accession: JH0168
 A:Molecule type: DNA
 A:Residues: 1-180, 'G', 182-525 <SMA>
 A:Cross-references: GB:M31744; NID:g205104; PIDN:AAA1500.1; PID:g205105
 A:Experimental source: brain
 A>Note: only a list of differences from sequence S06708 is given
 R:Stuenkel, W.; Ruppersberg, J.P.; Schroeter, K.H.; Sakmann, B.; Stocker, M.; Giese, K.H.
 EMBO J. 8, 3235-3244, 1989
 A:Title: Molecular basis of functional diversity of voltage-gated potassium channels in
 A:Reference number: S06708; MUID:90059914
 A:Accession: S06708
 A:Molecule type: mRNA

A:Residues: 1-105, 'L', 107-180, 'G', 182-525 <STU>
 A:Cross-references: EMBL:X16001; NID:g57034; PIDN:CAA34132.1; PID:g57035
 C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane
 F:185-203/Domain: transmembrane #status predicted <TM1>
 F:245-266/Domain: transmembrane #status predicted <TM2>
 F:278-298/Domain: transmembrane #status predicted <TM3>
 F:313-331/Domain: transmembrane #status predicted <TM4>
 F:348-367/Domain: transmembrane #status predicted <TM5>
 F:383-392/Domain: transmembrane beta strand #status predicted <TM6>
 F:393-401/Domain: transmembrane beta strand #status predicted <TM7>
 F:409-431/Domain: transmembrane #status predicted <TM8>
 F:470/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pre

Query Match 91.0%; Score 71; DB 2; Length 525;
 Best Local Similarity 86.7%; Pred. No. 0.0001;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 FAEADDPPTSGFSSIP 15
 |||||||

Db 368 FAEADDPSSGFNSIP 382

RESULT 5
 I84205
 potassium channel protein MK3 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C:Accession: C40090; I84205
 R:Chandy, K.G.; Williams, C.B.; Spencer, R.H.; Aguilar, B.A.; Chanshanl, S.; Tempel,
 Science 247, 973-975, 1990
 A:Title: A family of three mouse potassium channel genes with intronless coding regio
 A:Reference number: A40090; MUID:90161996
 A:Accession: C40090
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-528 <CHA>
 A:Cross-references: GB:M30441; NID:g199712; PIDN:AAA39716.1; PID:g199713

Query Match 91.0%; Score 71; DB 2; Length 528;
 Best Local Similarity 86.7%; Pred. No. 0.0001;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 FAEADDPPTSGFSSIP 15
 |||||||

Db 371 FAEADDPSSGFNSIP 385

RESULT 6
 S09045
 potassium channel protein MK-4 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
 C:Accession: S09045
 R:Betsholtz, C.; Baumann, A.; Kenna, S.; Ashcroft, F.M.; Ashcroft, S.J.H.; Berggren,
 FEBS Lett. 263, 121-126, 1990
 A:Title: Expression of voltage-gated K⁺ channels in insulin-producing cells. Analysis
 A:Reference number: S09042; MUID:90235950
 A:Accession: S09045
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-57 <BET>

Query Match 80.8%; Score 63; DB 2; Length 57;
 Best Local Similarity 80.0%; Pred. No. 0.0002;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 FAEADDPPTSGFSSIP 15
 |||||||

Db 11 FAEADDPTRHQSIP 25

RESULT 7

A39922 potassium channel KCNA4 - human

N:Alternate names: potassium channel HK1; potassium channel PCN2; shaker-related potassium channel HK1; Homo sapiens (man)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 05-Nov-1999

C:Accession: A39922; S12630; I77465

R:Ramashanti, M.M.; Knoch, K.M.; Walbridge, J.A.; Kroeber, H.; Roden, D.M.; Glover, D.M.

FASEB J. 5, 331-337, 1991

A:Title: Molecular cloning and characterization of two voltage-gated K(+) channel cDNAs

A:Reference number: A39922; MUID:91160866

A:Accession: A39922

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-653 <TAM>

A:Cross-references: GB:M60450; NID:9308762; PIDN:AAA61275.1; PID:9308763

R:Phillipson, L.H.; Schaefer, K.; Lamendola, J.; Bell, G.I.; Steiner, D.F.

Nucleic Acids Res. 18, 7160, 1990

A:Title: Sequence of a human fetal skeletal muscle potassium channel cDNA related to RCK

A:Reference number: S12630; MUID:91088321

A:Accession: S12630

A:Molecule type: mRNA

A:Residues: 1-37, 'R', '39-41', 'R', '43-83', 'EEAT', '89-303', 'D', '305-541', 'V', '543-630', 'A', '632-653

A:Cross-references: EMBL:M55514; NID:9189659; PIDN:AAA60034.1; PID:9189660

R:Ramashanti, M.; Gautam, M.; Kamb, A.A.; Rudy, B.; Tanouye, M.A.; Mathew, M.K.

Mol. Cell. Neurosci. 1, 214-223, 1990

A:Title: Human potassium channel genes: molecular cloning and functional expression.

A:Reference number: I77465

A:Accession: I77465

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-653 <RES>

A:Cross-references: GB:L02751; NID:9186666; PIDN:AAA36140.1; PID:9186667

C:Genetics:

A:Gene: GDB:KCNA4

A:Cross-references: GDB:126730; OMIM:176266

A:Map position: 11p14-11p14

C:Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; volt

Query Match 75.6%; Score 59; DB 2; Length 653;

Best Local Similarity 73.3%; Pred. No. 0.018; Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAADPTSGFSSIP 15

DB 498 FAADPTTHFOSIP 512

RESULT 8

S11049 potassium channel protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999

C:Accession: S11049

R:Tseng-Crank, J.C.L.; Tseng, G.N.; Schwartz, A.; Tanouye, M.A.

FEBS Lett. 268, 63-68, 1990

A:Title: Molecular cloning and functional expression of a potassium channel cDNA isolate

A:Reference number: S11049; MUID:9046174

A:Accession: S11049

A:Molecule type: mRNA

A:Residues: 1-654 <TSE>

A:Cross-references: GB:M32867; NID:9205042; PIDN:AAA41469.1; PID:9205043

Query Match 75.6%; Score 59; DB 2; Length 654;

Best Local Similarity 73.3%; Pred. No. 0.018; Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAADPTSGFSSIP 15

DB 499 FAADPTTHFOSIP 513

RESULT 9

E39113 potassium channel KVL4 - rat

N:Alternate names: potassium channel RK3; shaker-related potassium channel RCK4

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 05-Nov-1999

C:Accession: E39113; S06710

R:Roberts, S.L.; Tamkun, M.M.

Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991

A:Title: Cloning and tissue-specific expression of five voltage-gated potassium chan

A:Reference number: A39113; MUID:91156594

A:Accession: E39113

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: mRNA

A:Residues: 1-654 <ROB>

R:Stuehmer, M.; Ruppersberg, J.P.; Schroeter, K.H.; Sakmann, B.; Stocker, M.; Giese, E.MBO J. 8, 3235-3244, 1989

A:Title: Molecular basis of functional diversity of voltage-gated potassium channels

A:Reference number: S06708; MUID:90059914

A:Accession: S06710

A:Molecule type: mRNA

A:Residues: 1-41, 'A', '43-83', 'EEAT', '89-94', 'K', '95-654 <STU>

A:Cross-references: EMBL:X16002; NID:957036; PIDN:CAA34133.1; PID:957037

C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane

F:309-327/Domain: transmembrane #status predicted <TM1>

F:372-393/Domain: transmembrane #status predicted <TM2>

F:405-424/Domain: transmembrane #status predicted <TM3>

F:425-462/Domain: transmembrane #status predicted <TM4>

F:479-498/Domain: transmembrane #status predicted <TM5>

F:514-523/Domain: transmembrane beta strand #status predicted <TM6>

F:524-532/Domain: transmembrane beta strand #status predicted <TM7>

F:540-562/Domain: transmembrane #status predicted <TM8>

F:533/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:600/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pre

Query Match 75.6%; Score 59; DB 2; Length 654;

Best Local Similarity 73.3%; Pred. No. 0.018; Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAADPTSGFSSIP 15

DB 499 FAADPTTHFOSIP 513

RESULT 10

S24125 potassium channel protein - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C:Accession: S24125

R:Garcia-Guzman, M.; Calvo, S.; Cena, V.; Criado, M.

FEBS Lett. 308, 283-289, 1992

A:Title: Molecular cloning and permanent expression in a neuroblastoma cell line of a

A:Reference number: S24125; MUID:92371645

A:Accession: S24125

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-660 <GAR>

A:Cross-references: EMBL:X57033; NID:9646; PIDN:CAA40349.1; PID:9647

Query Match 75.6%; Score 59; DB 2; Length 660;

Best Local Similarity 73.3%; Pred. No. 0.018; Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAADPTSGFSSIP 15

DB 506 FAADPTTHFOSIP 520

```

RESULT 11
S09049
Potassium channel protein Hak-7 - hamster (fragment)
C:Species: Cricetinae gen. sp. (hamster)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C:Accession: S09049
R:Betsholtz, C.; Baumann, A.; Kenna, S.; Ashcroft, F.M.; Ashcroft, S.J.H.; Berggren, P.O.
FEBS Lett. 263, 121-126, 1990
A:Title: Expression of voltage-gated K+ channels in insulin-producing cells. Analysis by
A:Reference number: S09042; MUID:90235950
A:Accession: S09049
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-49 <BET>

Query Match          64.1%; Score 50; DB 2; Length 49;
Best Local Similarity 73.3%; Pred. No. 0.034;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAEADPTGFSFSSIP 15
      ||||| 1 |||||
Db 3 FAEADNCGSHFSSIP 17

RESULT 12
S12787
Potassium channel KCNA2 - human
N:Alternate names: potassium channel HBK2
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: S12787; S15057
R:Gupe, A.; Schroeder, K.H.; Ruppersberg, J.P.; Stocker, M.; Drewes, T.; Beckh, S.; Por
EMBO J. 9, 1749-1756, 1990
A:Title: Cloning and expression of a human voltage-gated potassium channel. A novel mem
A:Reference number: S12786; MUID:90269208
A:Accession: S12787
A:Molecule type: mRNA
A:Residues: 1-529 <GRU>
A:Cross-references: EMBL:X17622
R:Pongs, O.
submitted to the EMBL Data Library, November 1989
A:Reference number: S15057
A:Accession: S15057
A:Molecule type: mRNA
A:Residues: 1-57, 'T', '59-529 <PON>
A:Cross-references: EMBL:X17622; NID:932032; PIDN:CAA35623.1; PID:932033
C:Genetics:
A:Gene: GDB:KCNA2; HK4; KVL2
A:Cross-references: GDB:128062; OMIM:176262
C:Keywords: glycoprotein; ion channel; transmembrane protein
F:175-193/Domain: transmembrane #status predicted <TM1>
F:263-384/Domain: transmembrane #status predicted <TM2>
F:263-316/Domain: transmembrane #status predicted <TM3>
F:340-359/Domain: transmembrane #status predicted <TM4>
F:376-395/Domain: transmembrane #status predicted <TM5>
F:457-458/Domain: transmembrane #status predicted <TM6>

Query Match          62.8%; Score 49; DB 2; Length 529;
Best Local Similarity 73.3%; Pred. No. 0.04;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 FAEADPTGFSFSSIP 15
      ||||| 1 |||||
Db 396 FAEADDDSLFSPSP 410

RESULT 13
JH0166
potassium voltage-gated channel - rat
N:Alternate names: potassium channel RK4; shaker-related potassiu
C:Species: Rattus norvegicus (Norway rat)

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 05-Nov-1999
C:Accession: JH0166; D39113; I55392
R:Swanson, R.; Marshall, J.; Smith, J.S.; Williams, J.B.; Boyle, M.B.; Folander, K.;
Neuron 4, 929-939, 1990
A:Title: Cloning and expression of cDNA and genomic clones encoding three delayed rec
A:Reference number: JH0166; MUID:90297965
A:Accession: JH0166
A:Molecule type: mRNA
A:Residues: 1-602 <SWA>
A:Cross-references: GB:M27158; NID:9205100; PIDN:AAA41498.1; PID:9205101
R:Experimental source: brain
R:Roberts, S.L.; Tamkun, M.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
A:Title: Cloning and tissue-specific expression of five voltage-gated potassium chann
A:Reference number: A39113; MUID:91156694
A:Accession: D39113
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:Molecule type: mRNA
A:Residues: 1-552, 'S', '554-602 <ROB>
R:Morl, Y.; Matsubara, H.; Folco, E.; Siegel, A.; Koren, G.
J. Biol. Chem. 268, 26482-26493, 1993
A:Title: The transcription of a mammalian voltage-gated potassium channel is regulate
A:Reference number: I55392; MUID:94075338
A:Accession: I55392
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-15 <RES>
A:Cross-references: GB:L23434; NID:9443766; PIDN:AAA42337.1; PID:9443767
C:Experimental source: Sprague-Dawley
C:Genetics:
A:Gene: KVL5
C:Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; v
F:242-260/Domain: transmembrane #status predicted <TM1>
F:316-336/Domain: transmembrane #status predicted <TM2>
F:347-368/Domain: transmembrane #status predicted <TM3>
F:387-408/Domain: transmembrane #status predicted <TM4>
F:423-444/Domain: transmembrane #status predicted <TM5>
F:484-505/Domain: transmembrane #status predicted <TM6>
F:10,44,116,181,290/Binding site: carboxylate (Asn) (covalent) #status predicted
F:81,535,546,569/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match          62.8%; Score 49; DB 2; Length 602;
Best Local Similarity 73.3%; Pred. No. 0.07;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAEADPTGFSFSSIP 15
      ||||| 1 |||||
Db 443 FAEADNCGSHFSSIP 457

RESULT 14
S09042
potassium channel protein MK-1 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C:Accession: S09042
R:Betsholtz, C.; Baumann, A.; Kenna, S.; Ashcroft, F.M.; Ashcroft, S.J.H.; Berggren,
FEBS Lett. 263, 121-126, 1990
A:Title: Expression of voltage-gated K+ channels in insulin-producing cells. Analysis
A:Reference number: S09042; MUID:90235950
A:Accession: S09042
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-57 <BET>

Query Match          61.5%; Score 48; DB 2; Length 57;
Best Local Similarity 66.7%; Pred. No. 0.092;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAEADPTGFSFSSIP 15
      ||||| 1 |||||

```


Db 11 FAAEFEAFSHFSSIP 25

RESULT 15

S09043

potassium channel protein MK-2 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993

C:Accession: S09043

R:Beuscholtz, C.; Baumann, A.; Kenna, S.; Ashcroft, F.M.; Ashcroft, S.J.H.; Berggren, P.O.

FEBS Lett. 263, 121-126, 1990

A:Title: Expression of voltage-gated K⁺ channels in insulin-producing cells. Analysis by

A:Reference number: S09042; MUID:90235950

A:Accession: S09043

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-57 <BET>

Query Match

61.5%; Score 48; DB 2; Length 57;

Best Local Similarity 73.3%; Pred.No. 0.092;

Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 FAADDPTGFSFSSIP 15

||||| | | | |

DB 11 FAADDVDSLFSIP 25

Search completed: February 2, 2001, 10:37:14
Job time: 87 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:38:03 ; Search time 45.64 Seconds
(without alignments)
11.238 Million cell updates/sec

Title: US-09-273-217-4
Perfect score: 78
Sequence: 1 FAHADPTSCFSSIP 15

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues
Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries.

Database :

A.Geneseq.36:*

- 1: /SIDSI/gcgdata/geneseq/geneseqp/AA1980.DAT:*
- 2: /SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseqp/AA1982.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseqp/AA1983.DAT:*
- 5: /SIDSI/gcgdata/geneseq/geneseqp/AA1984.DAT:*
- 6: /SIDSI/gcgdata/geneseq/geneseqp/AA1985.DAT:*
- 7: /SIDSI/gcgdata/geneseq/geneseqp/AA1986.DAT:*
- 8: /SIDSI/gcgdata/geneseq/geneseqp/AA1987.DAT:*
- 9: /SIDSI/gcgdata/geneseq/geneseqp/AA1988.DAT:*
- 10: /SIDSI/gcgdata/geneseq/geneseqp/AA1989.DAT:*
- 11: /SIDSI/gcgdata/geneseq/geneseqp/AA1990.DAT:*
- 12: /SIDSI/gcgdata/geneseq/geneseqp/AA1991.DAT:*
- 13: /SIDSI/gcgdata/geneseq/geneseqp/AA1992.DAT:*
- 14: /SIDSI/gcgdata/geneseq/geneseqp/AA1993.DAT:*
- 15: /SIDSI/gcgdata/geneseq/geneseqp/AA1994.DAT:*
- 16: /SIDSI/gcgdata/geneseq/geneseqp/AA1995.DAT:*
- 17: /SIDSI/gcgdata/geneseq/geneseqp/AA1996.DAT:*
- 18: /SIDSI/gcgdata/geneseq/geneseqp/AA1997.DAT:*
- 19: /SIDSI/gcgdata/geneseq/geneseqp/AA1998.DAT:*
- 20: /SIDSI/gcgdata/geneseq/geneseqp/AA1999.DAT:*
- 21: /SIDSI/gcgdata/geneseq/geneseqp/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	15	20	Y42765 Rat potassium chan
2	48.5	62.2	476	20	Y28674 Arabidopsis GRP cy
3	48	61.5	495	20	Y32014 Human cation chan
4	46	59.0	15	20	Y42762 Rat potassium chan
5	43	55.1	597	12	R12384 Bovine pancreatic
6	41	52.6	49	13	R28600 Sequence of a modi
7	41	52.6	78	15	R62361 Synthetic "King Ko
8	41	52.6	78	16	R80094 Synthetic "King Ko
9	41	52.6	575	13	R30045 gE gene deletion f
10	41	52.6	575	15	R47175 Sequence of polype
11	41	52.6	575	16	R82214 Bovine herpesvirus
12	41	52.6	617	14	R31956 Sequence encoded b

13	41	52.6	617	16	R79036
14	40	51.3	535	15	R58985
15	40	51.3	538	16	R75098
16	40	51.3	538	17	W10058
17	40	51.3	546	15	R58981
18	40	51.3	568	15	R58982
19	40	51.3	568	17	R99258
20	40	51.3	668	15	R58983
21	40	51.3	668	15	R70145
22	40	51.3	722	15	R58984
23	40	51.3	722	16	R75107
24	40	51.3	722	17	W10050
25	40	51.3	722	17	R98926
26	40	51.3	742	12	R14311
27	40	51.3	742	17	R98927
28	40	51.3	744	15	R45189
29	40	51.3	745	13	R20098
30	40	51.3	745	15	R58980
31	40	51.3	745	17	R99257
32	40	51.3	745	20	Y32168
33	40	51.3	858	20	Y32015
34	39	50.0	51	14	R38802
35	39	50.0	77	14	R38797
36	39	50.0	454	20	Y34779
37	39	50.0	490	20	Y34121
38	39	50.0	491	21	Y70454
39	39	50.0	491	21	Y53780
40	39	50.0	616	20	Y32013
41	38	48.7	109	21	Y64595
42	38	48.7	267	19	W81726
43	38	48.7	267	19	W64359
44	38	48.7	267	20	Y39156
45	38	48.7	267	20	Y39013

ALIGNMENTS

RESULT 1
Y42765 standard; peptide: 15 AA.
XX
AC Y42765;
XX
DT 20-DEC-1999 (first entry)
XX
DE Rat potassium channel Kv1.3 vestibule-derived peptide #4.
XX
KW Ion channel; potassium channel; vestibule; inhibitor; antibody;
KW polyclonal; antagonist; hypertension; cardiac ischemia;
KW bronchial constriction; neurological diseases.
XX
XX Synthetic.
OS Rattus sp.
XX
PM W09948927-A1.
XX
PD 30-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06019.
XX
PR 25-MAR-1998; 98US-0079268.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Huang X;
XX
DR WPI; 1999-601205/51.
XX
PT Designing specific blockers that bind to the external vestibule region
PT of ion channels, potentially useful for treating e.g. hypertension
XX
PS Claim 9; Page 9; 40pp; English.

Infectious bovine
Bile salt-stimulat
Recombinant bile s
Human wild-type bi
Bile salt-stimulat
Bile salt-stimulat
Human bile salt-st
Bile salt-stimulat
Bile salt-stimulat
Bile salt-stimulat
Human bile salt-ac
Human milk bile-sa
Human bile salt-ac
BSSL/CEL. Homo sa
Bile-salt stimulat
Bile salt-stimulat
Human bile salt-st
Human bile salt-st
Human cation chann
King Kong conotoxi
Conotoxin preprope
Chlamydia pneumoni
Human potassium ch
Human membrane cha
A human voltage-ga
Drosophila melanog
Nonclassical cadhe
M. tuberculosis im
Mycobacterium tube
M. tuberculosis an
M. tuberculosis re

XX This sequence represents a peptide (#4), derived from the
 CC extracellular vestibule portion of the rat potassium channel Kv1.3.
 CC This was conjugated to keyhole limpet haemocyanin (KLH) and used to
 CC generate polyclonal antibodies. The vestibule portion of potassium
 CC channels is located on the extracellular portion of the channel protein,
 CC and generally comprises a loop between the S5 transmembrane domain and
 CC the pore forming region of the channel, or between the pore forming
 CC region and the S6 transmembrane domain. The antibodies generated against
 CC vestibule peptides act as potassium channel inhibitors by binding to the
 CC vestibule portion, physically blocking the pore, or otherwise inducing a
 CC conformational change in the channel. These potassium channel blockers
 CC are potential therapeutic agents for e.g., hypertension, cardiac
 CC ischaemia, bronchial constriction and neurological diseases. Such
 CC inhibitors are specific for particular types of ion channel, and
 CC are produced by rational design based on known nucleotide and amino acid
 CC sequences for ion channels.

XX Sequence 15 AA:

Query Match 100.0%; Score 78; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.4e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAEADPTSGFSSIP 15
 ID 1 faeaddptsgfssip 15

RESULT 2
 Y28674 standard; Protein; 476 AA.

XX Y28674;

XX 26-OCT-1999 (first entry)

XX Arabidopsis GTP cyclohydrolase II/DHP synthase.

XX Bifunctional enzyme; GTP cyclohydrolase II; DHP synthase; herbicide;
 KM 3,4-dihydroxy-2-butanone-4-phosphate synthase; riboflavin biosynthesis;
 KM 2,5-diamino-4-oxy-6-ribosylamino-pyrimidine-5-phosphate; GTP; Shuffled;
 KM ribulose-5-phosphate; 3,4-dihydroxy-2-butanone phosphate; inhibitor;
 KM Arabidopsis thaliana Expressed Sequence Tag database; Bacillus subtilis;
 KM enhanced tolerance.

XX Arabidopsis thaliana.

XX MO9938986-A2.

XX 05-AUG-1999.

XX 28-JAN-1999; 99MO-EP00556.

XX 30-JAN-1998; 98US-0109810.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERFINDUNGEN VERM GES MBH.

XX Bruun SA, Guyer CD, Johnson MA, Volrath SL, Ward ER.

XX WPI; 1999-479193/40.

XX N-PSDB; X80820.

XX New isolated riboflavin biosynthesis genes, used to identify

XX compounds for use, e.g. as herbicides

XX Claim 49; Page 71-73; 78pp; English.

XX The present sequence is bifunctional enzyme GTP cyclohydrolase II/
 CC 3,4-dihydroxy-2-butanone-4-phosphate synthase (DHP synthase). GTP cyclo
 CC -hydrolase II is the first enzyme of riboflavin biosynthesis, catalysing

CC the synthesis of 2,5-diamino-4-oxy-6-ribosylamino-pyrimidine-5-phosphate
 CC from GTP. DHP synthase catalyses the conversion of ribulose 5 phosphate
 CC to 3,4-dihydroxy-2-butanone phosphate (DHP). A cDNA sequence was derived
 CC from Arabidopsis thaliana Expressed Sequence Tag database and showed
 CC homology to the bifunctional GTP cyclohydrolase II/DHP synthase of
 CC Bacillus subtilis. The purified enzyme can be used to screen for novel
 CC inhibitors which can be used as herbicides to suppress the
 CC growth of undesirable vegetation. The encoding nucleotide sequence can
 CC be shuffled to produce an enzyme that confers on plants, enhanced
 CC tolerance to herbicides in an amount that normally inhibits riboflavin
 CC biosynthesis. This can be used to selectively suppress the growth of
 CC weeds.

XX Sequence 476 AA:

Query Match 62.2%; Score 48.5; DB 20; Length 476;
 Best Local Similarity 63.2%; Pred. No. 0.64;
 Matches 12; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

QY 2 AEADPTSGFSSIP 15
 ID 2 aeaddptsgfssip 15

RESULT 3
 Y32014 standard; Protein; 495 AA.

XX Y32014;

XX 05-JAN-2000 (first entry)

XX Human cation channel protein.

XX DE

XX Cation channel protein; CCP; ion transport; arrhythmia;
 KM diabetes mellitus; seizure; asthma; hypertension; therapy;
 KM protein engineering; human.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 61..119 /note="crystal region"

XX MO9947923-A2.

XX 23-SEP-1999.

XX 22-MAR-1999; 99MO-US06307.

XX 20-MAR-1998; 98US-0045529.

XX 02-APR-1998; 98US-0054347.

XX (UYRQ) UNIV ROCKEFELLER.

XX Mackinnon R;

XX WPI; 1999-601131/51.

XX Assays for screening compounds which interact with cation channel

XX proteins, useful for providing agents for treatment of diseases

XX Claim 21; Page 135-137; 165pp; English.

XX The present sequence represents a human cation channel protein
 CC (CCP). The invention provides an assay for screening potential
 CC drugs or agents which interact with CCPs using prokaryotic CCPs
 CC (such as those given in Y32009-12) mutated, using recombinant DNA
 CC technology, to mimic the physiological function and chemical

XX properties of a functional eukaryotic CCP (such as those given in
 CC Y32013-22). An example of a mutated prokaryotic CCP is given in
 CC Y32024. The crystal region of the CCP may also be used in the

CC assay. The drugs or agents obtained can be used to treat
 CC conditions related to the function of CCP in vivo, such as cardiac
 CC arrhythmia, diabetes mellitus, seizure disorder, asthma or
 CC hypertension. The invention has overcome the physical limitations
 CC regarding the isolation and purification of eukaryotic CCPs.

SQ Sequence 495 AA;

Query Match 61.5%; Score 48; DB 20; Length 495;
 Best Local Similarity 66.7%; Pred. No. 0.83;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 FAEADPTSGFSSIP 15
 |||||:|||||
 Db 346 faaeaeashssip 360

RESULT 4

Y42762 Y42762 standard; peptide: 15 AA.

AC Y42762;

DT 20-DEC-1999 (first entry)

DE Rat potassium channel Kv1.2 vestibule-derived peptide #1.

XX Ion channel; potassium channel; vestibule; inhibitor; antibody;

KM polyclonal; antagonist; hypertension; cardiac ischemia;

KW bronchial constriction; neurological diseases.

XX Synthetic.

OS Rattus sp.

PN W09948927-A1.

XX 30-SEP-1999.

PF 19-MAR-1999; 99WO-US06019.

XX 25-MAR-1998; 98US-0079268.

XX (CORR) CORNELL RES FOUND INC.

XX Huang X;

DR WPI: 1999-601205/51.

XX Designing specific blockers that bind to the external vestibule region

PT of ion channels, potentially useful for treating e.g. hypertension

XX Claim 9; Page 8; 40pp; English.

XX This sequence represents a peptide (#1), derived from the extracellular

CC vestibule portion of the rat delayed rectifier potassium channel Kv1.2.

CC This was conjugated to keyhole limpet haemocyanin (KLH) and used to

CC generate polyclonal antibodies. The vestibule portion of potassium

CC channels is located on the extracellular portion of the channel protein,

CC and generally comprises a loop between the S5 transmembrane domain and

CC the pore forming region of the channel, or between the pore forming

CC region and the S6 transmembrane domain. The antibodies generated against

CC vestibule peptides act as potassium channel inhibitors by binding to the

CC vestibule portion, physically blocking the pore, or otherwise inducing a

CC conformational change in the channel. These potassium channel blockers

CC are potential therapeutic agents for e.g., hypertension, cardiac

CC ischemia, bronchial constriction and neurological diseases. Such

CC inhibitors are specific for particular types of ion channel, and

CC are produced by rational design based on known nucleotide and amino acid

CC sequences for ion channels.

CC Sequence 15 AA;

Query Match 59.0%; Score 46; DB 20; Length 15;
 Best Local Similarity 66.7%; Pred. No. 0.034;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 FAEADPTSGFSSIP 15
 |||||:|||||
 Db 1 faeaderdsqfssip 15

RESULT 5

ID R12384 R12384 standard; Protein: 597 AA.

AC R12384;

DT 14-AUG-1991 (first entry)

DE Bovine pancreatic cholesterol esterase.

XX Cholesterol; PCE; atherosclerosis.

OS Bos taurus.

PN W09107483-A.

XX 30-MAY-1991.

PF 13-NOV-1990; 90WO-US06483.

XX 13-NOV-1989; 89US-0434899.

XX (LANG/) LANGE L G.

PI Lange LG, Spillburg CA;

DR WPI: 1991-178095/24.

XX N-PSDB; Q11977.

PT Method for purifying pancreatic cholesterol esterase - gene

PT encoding it for expression in cells used e.g. to screen

XX inhibitors, decrease cholesterol absorption, etc.

XX Disclosure: fig 1; 28pp; English.

XX This recombinant bovine pancreatic cholesterol esterase (PCE) is

CC purified to homogeneity (claimed) using a sulphated matrix. It

CC can be used to produce esterified cholesterol from free fatty

CC acids and free cholesterol or to break down cholesteryl-fatty

CC acids by altering the taurocholate concn. Thus it can be used

CC to alter the cholesterol/cholesterol ester compsn. of food

CC stuffs and biologics. It can also be used to produce antibodies

CC (e.g. by immunising cows and purifying the antibodies from their

CC milk) which can be used as inhibitors to PCE which may lead to

CC reduced serum cholesterol levels.

CC See also Q11978-79 and R12385-86.

XX Sequence 597 AA;

Query Match 55.1%; Score 43; DB 12; Length 597;

Best Local Similarity 46.7%; Pred. No. 8.5;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 FAEADPTSGFSSIP 15

Db 489 fatgqpnctnscvp 503

RESULT 6

R28600 R28600 standard; Protein: 49 AA.

AC	R28600;
XX	
DT	21-MAR-1993 (first entry)
XX	
DE	Sequence of a modified filamentous phage coat protein membrane anchor
DE	cpvIII.
XX	
KM	Filamentous phage; coat protein membrane anchor; cpvIII.
XX	
OS	Filamentous phage.
XX	
PN	WO9218619-A.
XX	
PD	29-OCT-1992.
XX	
PE	10-APR-1992; 92WO-US03091.
XX	
PR	10-APR-1991; 91US-0683602.
XX	
PR	27-JAN-1992; 92US-0826623.
XX	
PA	(SCRT) SCRIPPS RES INST.
XX	
PI	Barbas C, Kang A, Lerner RA;
XX	
DR	WPI; 1992-382106/46.
XX	
PT	Filamentous phage expressing heterodimeric receptor - esp.
XX	
PT	antibody, in its coat protein, useful for diagnostic assay, also
XX	
PS	new phage DNA libraries and mutagenic oligo:nucleotide primers
XX	
PS	Example; Page 187; 229pp; English.
XX	
CC	M3mp18 was used as a source for isolating the gene encoding
CC	cpvIII. The sequence of the gene encoding the membrane anchor
CC	domain of cpvIII (see Q30709) was modified through PCR
CC	amplification to incorporate the restriction endonuclease sites
CC	Spe I and EcoR I and two stop codons prior to the EcoR I site.
CC	The corresp. amino acid residue sequence of the membrane anchor
CC	domain of cpvIII is given in R28600.
XX	
Sequence	49 AA;
XX	

Query Match	52.6%	Score 41	DB 13	Length 49	
Best Local Similarity	53.8%	Pred. No. 1.1			
Matches	7	Conservative	2	Mismatches	4
				Indels	0
				Gaps	0
OY	2	A EADDP TSG FSSI	14		
Db	1	aegddp akafnsl	13		
RESULT	7				
R62361					
ID	R62361	standard; Protein; 78	AA.		
XX					
AC	R62361:				
XX					
DT	04-MAY-1995	(first entry)			
XX					
DE	Synthetic "King Kong" (KK-O)	conotoxin.			
XX					
KW	Conotoxin; toxin; insecticide; Baculovirus; gastropod; neurotoxin;				
KW	Conus textile; KK-O.				
XX					
OS	Synthetic.				
XX					
PN	GB2276622-A.				
XX					
PD	05-OCT-1994.				
XX					
PF	25-MAR-1994;	94GB-0006032.			
XX					

PR	26-MAR-1993;	93GB-0006295.
XX		
PA	(GUES/)	GUEST P J.
PA	(ZENE)	ZENECA LTD.
XX		
PI	Earley FGP,	Guest FU, Suner M, Windass JD;
XX		
DR	WPI; 1994-296384/37.	
DR	N-Psdb; Q73314,	Q73320.
XX		
PT	New synthetic DNA encoding mollusc-derived insecticidal toxin -	
PT	and related transfer vectors, host cells and plants; useful as	
PT	biological insect control agents	
XX		
PS	Claim 1: Figure 1; 75pp; English.	
XX		
CC	The conotoxins are low molecular weight neuroactive peptides	
CC	isolated from the Conus genus of marine gastropods. They have a	
CC	very diverse range of biological effects. Some of these conotoxins	
CC	exhibit insecticidal activity. This synthetic sequence of the Conus	
CC	textile derived protein Kk-O was expressed in Baculovirus (AcMNPV)	
CC	expression systems and was found to be capable of significantly	
CC	shortening the time a baculovirus takes to incapacitate susceptible	
CC	insect hosts.	
XX		
SQ	Sequence	78 AA;

Query Match	52.6%	Score 41	DB 15	Length 78
Best Local Similarity	50.0%	Pred. No. 1.9		
Matches	7	Conservative	3	Mismatches
			4	Indels
			0	Gaps
				0
QY	1	FAEADDP TSGFSFI 14		
		: :		
Db	19	fatcddgprnglgnl 32		
RESULT	8			
ID	R80094	standard; Protein; 78 AA.		
AC	R80094			
XX				
XX				
XX				
DT	09-MAY-1996	(first entry)		
DE	Synthetic "King Kong" (SKK-0) conotoxin.			
XX	Insecticidal; recombinant baculovirus; polyhedrin; heterologous;			
KM	gene; ACNMNV virus; King Kong; conotoxin gene; SKK-0.			
XX				
OS	Synthetic.			
XX				
PN	W09526410-A2.			
XX				
PD	05-OCT-1995.			
XX				
PF	27-MAR-1995; 95MO-GB00677.			
XX				
PR	25-MAR-1994; 94GB-0005951.			
XX				
PA	(ZENE) ZENECA LTD.			
XX				
PI	Windass JD;			
XX				
DR	WPI; 1995-351327/45.			
XX				
DR	N-PSDB; T04668.			
XX				
PT	New insecticidal recombinant baculovirus - comprises a polyhedron			
XX	gene and a heterologous gene expressing an insecticidal protein with			
XX	different promoters			
XX				
XX	Example 2; 31; 58pp; English.			

CC A novel insecticidal recombinant baculovirus comprises a polyhedrin
 CC gene and a heterologous gene, encoding an insecticidal protein,
 CC under the control of different promoters. A specific example is a
 CC recombinant AcMNPV virus carrying the synthetic "King Kong"
 CC conotoxin gene (SKK-O) T04668 (which encodes R80094) under the
 CC transcriptional control of the polyhedrin promoter, and an active
 CC polyhedrin gene under the control of the p10 promoter.

XX Sequence 78 AA:

Query Match 52.6%; Score 41; DB 16; Length 78;
 Best Local Similarity 50.0%; Pred. No. 1.9;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 AEADDPGSGFSSSI 14
 ||||| : :
 Db 19 fatadddprnglgnl 32

RESULT 9

R30045 R30045 standard; Protein; 575 AA.

AC R30045;

DT 29-APR-1993 (first entry)

DE gE gene deletion from mutant bovine herpes virus type 1.

KW BHV-1; cattle; cows; bos taurus; glycoprotein gene; vaccines;
 immunise; vaccinate; diagnosis; testing.

XX Bovine herpes virus type 1.

OS Key Location/Qualifiers

FT Region 1..26 /note="Eukaryotic export signal"

FT Region 423..450 /note="transmembrane region"

PN WO9221751-A.

PD 10-DEC-1992.

PF 05-JUN-1992; 92WO-NL00097.

PR 07-JUN-1991; 91NL-0000989.

PA (DIER-) STICHTING CENT DIERGENESKUNDIG INST.

XX Maes RK, Rijsewijk FAM, Van Oirschot JT;

DR WPI: 1992-433650/52.

DR N-NSDB; Q32857.

PT Mutant bovine herpes virus with deleted glyco-protein gene - used
 PT for vaccination against and diagnosis of bovine herpes virus type
 PT 1

PS Claim 1; Page 46; 84pp; English.

XX This sequence represents the area around a deletion of the gE gene
 CC in the Difivac-1 strain of bovine herpes virus type 1. It was
 CC decoded from the appropriate DNA, isolated as detailed in Q32857.
 CC Sequence analysis showed that this amino acid sequence has the
 CC characteristics of a transmembrane glycoprotein. The first 26 amino
 CC acids are recognised as a typically eukaryotic export signal and the
 CC area between 423 and 450 is recognised as a transmembrane region.
 CC In addition, three potential N-bound glycosylation sites occur in
 CC this sequence. This predicted amino acid sequence exhibits clear
 CC similarities to the glycoprotein gE-gene of herpes simplex virus
 CC (HSV). For this and other similarities found the gene is called the

CC BHV-1 gE gene.

XX Sequence 575 AA:

Query Match 52.6%; Score 41; DB 13; Length 575;
 Best Local Similarity 57.1%; Pred. No. 19;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 AEADDPGSGFSSIP 15
 ||||| : :
 Db 516 agapeptsgfarap 529

RESULT 10

R47175 R47175 standard; Protein; 575 AA.

AC R47175;

DT 20-JUL-1994 (first entry)

DE Sequence of polypeptide encoded by the second open reading frame in
 DE the unique short (US) region of bovine herpes virus (BHV) genome.

XX Insertion region; unique short region; US; vaccine; antigen.

XX Bovine herpes virus type 1, strain ST.

PN WO9400586-A.

PD 06-JAN-1994.

PF 25-JUN-1993; 93WO-FR00642.

PR 26-JUN-1992; 92FR-0007930.

PA (INMR) RHONE MERIEUX SA.

XX Audonnet JF, Legastelois ICMA, Leung-tack P, Riviere MEA;

DR WPI: 1994-026222/03.

DR N-PSDB; Q53350.

PT New insertion region sequence of bovine herpes virus genomic DNA
 PT - used for recombinant virus with this region deleted or
 PT inactivated, useful in vaccines allowing differentiation between
 PT vaccinated and infected cattle

PS Claim 9; Fig 2; 47pp; French.

XX The 4190 bp sequence in Q55350 encodes polypeptides homologous to
 CC HSV-1 gI, gE and US9; these are neither essential for in vitro
 CC replication nor important in inducing a protective immune response.
 CC It is genomic DNA purified from the ST strain of BHV-1. (BHV is also
 CC known as infectious bovine rhinotracheitis virus.) The sequence
 CC forms the insertion region in genomic DNA. RBHV in which the
 CC specific insertion region, esp. nucleotides 172-1311, has been
 CC deleted or inactivated by insertion are claimed.

XX Sequence 575 AA:

Query Match 52.6%; Score 41; DB 15; Length 575;
 Best Local Similarity 57.1%; Pred. No. 19;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 AEADDPGSGFSSIP 15
 ||||| : :
 Db 516 agapeptsgfarap 529

RESULT 11

```

R82214
ID R82214 standard; Protein; 575 AA.
XX
AC R82214;
XX
DT 10-APR-1996 (first entry)
XX
DE Bovine herpesvirus-1 FM gII glycoprotein.
XX
KM Glycoprotein, mutant; bovine herpesvirus; vaccine; antigen;
KW antigenic; bovine rhinotracheitis virus; IBRV; BHV; gII;
KM Immunisation; vaccination.
XX
OS Bovine herpesvirus.
XX
PN EP68356-A2.
XX
PD 23-AUG-1995.
XX
PF 31-JAN-1995; 95EP-0870007.
XX
PR 31-JAN-1994; 94ES-0000172.
XX
PA (HPR-) LAB HPRFA SA.
XX
PI Lloberas J, Perez-pons JA, Pinol J, Querol E, Rebordosa X;
PI
DR WPI: 1995-284793/38.
DR N-PSDB; T03824.
XX
PT New infectious bovine rhinotracheitis virus mutants - contain a
PT mutation in the glyco-protein gII gene, used to produce vaccines to
PT prevent infection
XX
PS Disclosure; Page 20-24; 33pp; English.
XX
CC The bovine herpesvirus-1 (BHV-1) FM gII glycoprotein gene can be
CC mutated by an insertion, deletion or substitution to produce a
CC BHV-1 FM gII- phenotype of an infectious bovine rhinotracheitis
CC virus (IBRV) which then fails to produce any antigenic gII
CC glycoprotein. These mutated viruses can then be used in vaccines
CC which are capable of eliciting both humoral and cellular responses
CC in the immunised animal. Vaccinated animals can be distinguished
CC serologically from animals infected with field strains of IBRV.
XX
SQ Sequence 575 AA;

```

```

Query Match 52.6%; Score 41; DB 16; Length 575;
Best Local Similarity 57.1%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

OY 2 AEADDPGSGSSIP 15
DB 516 agapeptsgfarap 529

RESULT 12
R31956
ID R31956 standard; Protein; 617 AA.
XX
AC R31956;
XX
DT 06-JUN-1993 (first entry)
XX
DE Sequence encoded by the IBR glycoprotein E gene.
XX
KM IBR glycoprotein E gene; unique short 2 gene.
XX
OS Infectious bovine rhinotracheitis.
XX
PN WO9302104-A.
XX

```

```

PD 04-FEB-1993.
XX
XX 20-JUL-1992; 92WO-US06034.
XX
PR 18-JUL-1991; 91US-0732584.
XX
PA (SYTR ) SYNTRO CORP.
XX
PI Cochran MD, Macdonald RD;
XX
DR WPI: 1993-058725/07.
DR N-PSDB; Q36769.
XX
XX
PT Recombinant infectious bovine rhinotracheitis virus - provides
PT isolated DNA encoding gPE glyco:protein, gPG glyco:protein and
PT unique short 2 genes of the virus
XX
XX Example; Fig 15; 240pp; English.
XX
XX The sequence of 2038 base pairs of the IBR unique short
CC region, starting approximately 1325 base pairs upstream in the
CC HindIII K/HindIII F junction in the HindIII K fragment, are shown.
CC The glycoprotein E (gPE) gene is transcribed toward the HindIII
CC K/HindIII F junction.
XX
XX
SQ Sequence 617 AA;

```

```

Query Match 52.6%; Score 41; DB 14; Length 617;
Best Local Similarity 57.1%; Pred. No. 21;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

OY 2 AEADDPGSGSSIP 15
DB 558 agapeptsgfarap 571

```

```

RESULT 13
R79036
ID R79036 standard; Protein; 617 AA.
XX
AC R79036;
XX
DT 15-APR-1996 (first entry)
XX

```

```

DE Infectious bovine rhinotracheitis virus glycoprotein E gene product.
XX
XX Bovine herpesvirus-1; infectious bovine rhinotracheitis virus;
KW IBR; bovine respiratory disease; shipping fever; vaccine; vector;
KW attenuation; glycoprotein E.
XX

```

```

OS Bovine herpesvirus-1 strain Cooper isolate S-IBR-000.
XX

```

```

FH Key Location/Qualifiers
FT Misc-difference 52 /note= "amino acid at position 52 is not
FT identified in the specification"
FT Misc-difference 458 /note= "amino acid at position 458 is not
FT identified in the specification"
XX

```

```

WO9521261-A1.
XX
PD 10-AUG-1995.
XX
PF 02-FEB-1995; 95WO-US01491.
XX
PR 04-FEB-1994; 94US-0191866.
XX
PA (SYTR ) SYNTRO CORP.
XX
PN Cochran MD;
XX

```


DR WPI; 1995-283781/37.
 DR N-PSDB; Q97671.
 XX
 PT Novel recombinant infectious bovine rhinotracheitis virus - used in
 PT vaccines to immunise animals against bovine respiratory disease
 PT complex
 XX
 PS Disclosure: Page 191-193; 301pp; English.
 XX
 CC The glycoprotein G (gE) (R79036) of infectious bovine rhinotracheitis
 CC (IBR) virus strain Cooper (isolate S-IBR-000) is encoded by DNA
 CC (Q97671) in plasmid PSY1645. Deletion of the gE gene attenuates IBR
 CC virus and provides a novel serological marker for differentiating the
 CC virus from wild-type virus. Novel foetal-safe, live, recombinant IBR
 CC viruses, e.g. S-IBR-052 (ATCC VR 2443), were constructed that were
 CC attenuated by deletion of the US2, gC and/or gE genes and which included
 CC DNA coding for infectious disease pathogen antigens. The recombinant
 CC vaccines are used to protect cattle against bovine respiratory disease
 CC complex (shipping fever).
 XX
 SQ Sequence 617 AA;
 Query Match 52.6%; Score 41; DB 16; Length 617;
 Best Local Similarity 57.1%; Pred. No. 21;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 OY 2 AEADPTSGFSSIP 15
 Db 558 agapeptsgfarap 571
 RESULT 14
 RS8985
 ID RS8985 standard; protein: 535 AA.
 XX
 AC RS8985;
 XX
 DT 03-MAY-1995 (first entry)
 XX
 DE Bile salt-stimulated lipase (variant A).
 XX
 KW Bile salt stimulated lipase: BSSL; glycoprotein; esterase;
 KW acetyl cholinesterase; cystic fibrosis; chronic pancreatitis;
 KW fat malabsorption; vitamins; dietary lipids; food supplement.
 XX
 OS Homo sapiens.
 XX
 PN WO9420610-A.
 XX
 PD 15-SEP-1994.
 XX
 PF 25-FEB-1994; 94WO-SE00160.
 XX
 PR 01-MAR-1993; 93SE-0000686.
 PR 04-MAR-1993; 93SE-0000722.
 XX
 PA (ASTR) ASTRA AB.
 XX
 PI Blackberg L, Edlund M, Hansson L, Herneil O, Lundberg L;
 PI Stromqvist M, Toernell J;
 XX
 DR WPI; 1994-303018/37.
 XX
 PT Bile salt-stimulated lipase variants and coding sequences - used
 PT to produce prods. for treatment of a pathological condition
 PT related to exocrine pancreatic insufficiency
 XX
 PS Example 1.1.2; Page 57-58; 102pp; English.
 XX
 CC Bile salt-stimulated lipase (BSSL) is a single chain glycoprotein
 CC which is highly glycosylated. The N-terminal half of the protein
 CC shows a homology to acetyl cholinesterase and some other esterases.

CC BSSL variant polypeptides can be used for the treatment of a
 CC pathological condition related to exocrine pancreatic insufficiency
 CC such as cystic fibrosis, chronic pancreatitis, fat malabsorption or
 CC malabsorption of fat soluble vitamins for improvement of utilisation
 CC of dietary lipids, particularly in preterm born infants. They can
 CC also be used as supplements for infant food formulations. The BSSL
 CC variants have maintained catalytic activity but contain less
 CC glycosylation sites than native BSSL. This variant is a deletion
 CC mutant lacking the C-terminal 187 amino acids of the wild-type
 CC protein (See R58980).
 CC
 XX
 SQ Sequence 535 AA;
 Query Match 51.3%; Score 40; DB 15; Length 535;
 Best Local Similarity 46.7%; Pred. No. 27;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 OY 1 FAEADPTSGFSSIP 15
 Db 471 fakgqpmgdsavp 485
 RESULT 15
 R75098
 ID R75098 standard; Protein: 538 AA.
 XX
 AC R75098;
 XX
 DT 26-JAN-1996 (first entry)
 XX
 DE Recombinant bile salt-activated lipase.
 XX
 KW Bile salt activated lipase; BAL; C-terminal repeat.
 XX
 OS Mammalia.
 XX
 PN JP07111891-A.
 XX
 PD 02-MAY-1995.
 XX
 PF 30-SEP-1993; 93JP-0245079.
 XX
 PR 30-SEP-1993; 93JP-0245079.
 XX
 PA (MEIP) MEIJI MILK PROD CO LTD.
 XX
 DR WPI; 1995-196318/26.
 DR N-PSDB; Q90569.
 XX
 PT New recombinant bile salt-activated lipase(s), DNA encoding them
 PT and vectors - useful for high level expression of the lipase(s) by
 PT fermenter-culturing.
 XX
 PS Claim 1; Page 9-10; 31pp; Japanese.
 XX
 CC New lipases are ones in which 1-15 repeats of any of the sequences
 CC R75099-R75105 (encoded by Q90570-Q90576) are attached to the C-
 CC terminus of the bile salt-activated lipase (BAL) of sequence R75098
 CC (encoded by Q90569) and/or in which the amino acid sequence SMRS
 CC (encoded by Q90578) is attached to the N-terminus of the BAL. The
 CC recombinant lipases can be produced by fermentation in *Pichia*
 CC pastoris GS 115 transformed host cells.
 XX
 SQ Sequence 538 AA;
 Query Match 51.3%; Score 40; DB 16; Length 538;
 Best Local Similarity 46.7%; Pred. No. 27;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 OY 1 FAEADPTSGFSSIP 15
 II: II I I::I

Fri Feb 2 15:15:38 2001

Db 471 faktgdpnmgdsavp 485

Search completed: February 2, 2001, 10:38:05
Job time: 138 sec

us-09-273-217-4.rag

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 2, 2001, 10:36:29 ; Search time 34.98 Seconds
(without alignments)
7.187 Million cell updates/sec

Title: US-09-273-217-3

Sequence: 1 GAQPNDSASEHTH 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6_COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/PCRTUS_COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	59.5	271	1	US-08-276-919-10 Sequence 10, Appl
2	47	59.5	271	1	US-08-776-088-13 Sequence 13, Appl
3	47	59.5	271	4	PCT-US95-09145A-13 Sequence 13, Appl
4	47	59.5	274	1	US-08-776-088-15 Sequence 15, Appl
5	47	59.5	274	4	PCT-US95-09145A-15 Sequence 15, Appl
6	47	59.5	325	1	US-08-276-919-4 Sequence 4, Appl
7	47	59.5	325	1	US-08-276-919-13 Sequence 13, Appl
8	47	59.5	325	1	US-08-776-088-4 Sequence 4, Appl
9	47	59.5	325	1	US-08-776-088-18 Sequence 18, Appl
10	47	59.5	325	4	PCT-US95-09145A-4 Sequence 4, Appl
11	47	59.5	325	4	PCT-US95-09145A-18 Sequence 18, Appl
12	47	59.5	354	1	US-08-276-919-2 Sequence 2, Appl
13	47	59.5	354	1	US-08-776-088-2 Sequence 2, Appl
14	47	59.5	354	1	US-08-776-088-6 Sequence 6, Appl
15	47	59.5	354	3	US-09-325-320-2 Sequence 2, Appl
16	47	59.5	354	4	PCT-US95-09145A-2 Sequence 2, Appl
17	47	59.5	354	4	PCT-US95-09145A-6 Sequence 6, Appl
18	47	59.5	434	1	US-08-337-602-2 Sequence 2, Appl
19	44	55.7	434	3	US-08-558-135-2 Sequence 2, Appl
20	38	48.1	98	2	US-08-454-557C-30 Sequence 30, Appl
21	38	48.1	98	2	US-08-340-426D-30 Sequence 30, Appl
22	38	48.1	98	2	US-08-450-673C-30 Sequence 30, Appl
23	38	48.1	98	2	PCT-US95-17111A-30 Sequence 30, Appl
24	37	46.8	266	2	US-07-857-224B-43 Sequence 43, Appl
25	37	46.8	267	2	US-07-857-224B-45 Sequence 45, Appl
26	37	46.8	3218	1	US-08-764-100-27 Sequence 27, Appl
27	36	45.6	302	3	US-08-303-861-20 Sequence 20, Appl
28	36	45.6	396	2	US-08-784-512-3 Sequence 3, Appl

29	36	45.6	403	2	US-09-092-770-4	Sequence 4, Appl
30	36	45.6	403	3	US-09-222-851-4	Sequence 4, Appl
31	36	45.6	488	2	US-08-928-692-11	Sequence 11, Appl
32	36	45.6	507	1	US-08-348-891A-3	Sequence 3, Appl
33	36	45.6	507	2	US-08-905-817-3	Sequence 3, Appl
34	36	45.6	543	1	US-08-362-232-2	Sequence 2, Appl
35	36	45.6	543	1	US-08-814-196-2	Sequence 2, Appl
36	36	45.6	631	1	US-08-605-541B-12	Sequence 12, Appl
37	35	44.3	42	1	US-08-664-449-39	Sequence 39, Appl
38	35	44.3	183	1	US-08-361-467B-11	Sequence 11, Appl
39	35	44.3	183	1	US-08-484-332C-11	Sequence 11, Appl
40	35	44.3	286	1	US-08-382-184-3	Sequence 3, Appl
41	35	44.3	286	2	US-08-641-356-3	Sequence 3, Appl
42	35	44.3	325	1	US-08-382-184-2	Sequence 2, Appl
43	35	44.3	325	2	US-08-641-356-2	Sequence 2, Appl
44	35	44.3	389	1	US-07-939-501A-1	Sequence 1, Appl
45	35	44.3	423	1	US-07-939-501A-10	Sequence 10, Appl

ALIGNMENTS

```
RESULT 1
US-08-276-919-10
; Sequence 10, Application US/08276919
; Patent No. 5589579
; GENERAL INFORMATION:
; APPLICANT: Torczynski, Richard M.
; APPLICANT: Bollon, Arthur P.
; TITLE OF INVENTION: Lung Cancer Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: TX
; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,919
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Neilligan, Mark C.
; REGISTRATION NUMBER: 36,389
; REFERENCE/DOCKET NUMBER: B35792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 214-939-4500
; TELEFAX: 214-939-4600
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-919-10
```

Query Match 59.5%; Score 47; DB 1; Length 271;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PNDPSASEHT 13
|||||
Db 96 PNDPSASEHT 105

RESULT 2

US-08-776-088-13
: Sequence 13, Application US/08776088
: Patent No. 5773579
: GENERAL INFORMATION:
: APPLICANT: Torczynski, Richard M.
: APPLICANT: Bollon, Arthur P.
: TITLE OF INVENTION: Lung Cancer Marker
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SIDLEY & AUSTIN
: STREET: 1201 Elm Street, Suite 4500
: CITY: Dallas
: STATE: TX
: COUNTRY: US
: ZIP: 75270-2197
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/776,088
: FILING DATE: 19-JUL-95
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Eugenia S. Hansen
: REGISTRATION NUMBER: 31,966
: REFERENCE/DOCKET NUMBER: 10365/05011
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 214-981-3300
: TELEFAX: 214-981-3400
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 271 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-776-088-13

Query Match 59.5%; Score 47; DB 1; Length 271;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PNDPSASEHT 13
|||||

Db 96 PNDPHGSEHT 105

RESULT 3
PCT-US95-09145A-13
: Sequence 13, Application PC/TUS9509145A
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Lung Cancer Marker
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
: STREET: 1201 Elm Street, Suite 4500
: CITY: Dallas
: STATE: TX
: COUNTRY: US
: ZIP: 75270-2197
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/09145A
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:

NAME: John A. Harre
: REGISTRATION NUMBER: 37,345
: REFERENCE/DOCKET NUMBER: B35792CIPCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 214-939-4500
: TELEFAX: 214-939-4600
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 271 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US95-09145A-13

Query Match 59.5%; Score 47; DB 4; Length 271;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PNDPSASEHT 13
|||||

Db 96 PNDPHGSEHT 105

RESULT 4
US-08-776-088-15
: Sequence 15, Application US/08776088
: Patent No. 5773579
: GENERAL INFORMATION:
: APPLICANT: Torczynski, Richard M.
: APPLICANT: Bollon, Arthur P.
: TITLE OF INVENTION: Lung Cancer Marker
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SIDLEY & AUSTIN
: STREET: 1201 Elm Street, Suite 4500
: CITY: Dallas
: STATE: TX
: COUNTRY: US
: ZIP: 75270-2197
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/776,088
: FILING DATE: 19-JUL-95
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Eugenia S. Hansen
: REGISTRATION NUMBER: 31,966
: REFERENCE/DOCKET NUMBER: 10365/05011
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 214-981-3400
: TELEFAX: 214-981-3300
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 274 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-776-088-15

Query Match 59.5%; Score 47; DB 1; Length 274;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PNDPSASEHT 13
|||||

Db 96 PNDPHGSEHT 105

RESULT 5
PCT-US95-09145A-15
Sequence 15, Application PC/TUS9509145A
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Lung Cancer Marker
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: TX
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09145A
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: John A. Harre
REGISTRATION NUMBER: 37,345
REFERENCE/DOCKET NUMBER: B35792CIPPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-09145A-15

Query Match 59.5%; Score 47; DB 4; Length 274;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
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Db 96 PNDPGESEHT 105

RESULT 6
US-08-276-919-4
Sequence 4, Application US/08276919
Patent No. 5589579
GENERAL INFORMATION:
APPLICANT: Torczynski, Richard M.
TITLE OF INVENTION: Lung Cancer Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: TX
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,919
FILING DATE:

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Neilligan, Mark C.
REGISTRATION NUMBER: 36,389
REFERENCE/DOCKET NUMBER: B35792
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-919-4

Query Match 59.5%; Score 47; DB 1; Length 325;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
|||||
Db 96 PNDPGESEHT 105

RESULT 7
US-08-276-919-13
Sequence 13, Application US/08276919
Patent No. 5589579
GENERAL INFORMATION:
APPLICANT: Torczynski, Richard M.
TITLE OF INVENTION: Lung Cancer Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: TX
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,919
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Neilligan, Mark C.
REGISTRATION NUMBER: 36,389
REFERENCE/DOCKET NUMBER: B35792
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-919-13

Query Match 59.5%; Score 47; DB 1; Length 325;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
|||||

Db 96 PNDPGESEHT 105

RESULT 8

US-08-776-088-4

Sequence 4, Application US/08776088,
Patent No. 5773579

GENERAL INFORMATION:

APPLICANT: Torczynski, Richard M.

APPLICANT: Bollon, Arthur P.

TITLE OF INVENTION: Lung Cancer Marker

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: SIDLEY & AUSTIN

STREET: 1201 Elm street, Suite 4500

CITY: Dallas

STATE: TX

COUNTRY: US

ZIP: 75270-2197

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,088

FILING DATE: 19-JUL-95

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Eugenia S. Hansen

REGISTRATION NUMBER: 31,966

REFERENCE/DOCKET NUMBER: 10365/05011

TELECOMMUNICATION INFORMATION:

TELEPHONE: 214-981-3300

TELEFAX: 214-981-3400

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 325 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-776-088-4

Query Match

Best Local Similarity 59.5%; Score 47; DB 1; Length 325;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPGESEHT 13

Db 96 PNDPGESEHT 105

RESULT 9

US-08-776-088-18

Sequence 18, Application US/08776088

Patent No. 5773579

GENERAL INFORMATION:

APPLICANT: Torczynski, Richard M.

APPLICANT: Bollon, Arthur P.

TITLE OF INVENTION: Lung Cancer Marker

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: SIDLEY & AUSTIN

STREET: 1201 Elm street, Suite 4500

CITY: Dallas

STATE: TX

COUNTRY: US

ZIP: 75270-2197

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,088

FILING DATE: 19-JUL-95

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Eugenia S. Hansen

REGISTRATION NUMBER: 31,966

REFERENCE/DOCKET NUMBER: 10365/05011

TELECOMMUNICATION INFORMATION:

TELEPHONE: 214-981-3300

TELEFAX: 214-981-3400

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 325 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-776-088-18

Query Match

Best Local Similarity 59.5%; Score 47; DB 1; Length 325;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPGESEHT 13

Db 96 PNDPGESEHT 105

RESULT 10

PCT-US95-09145A-4

Sequence 4, Application PC/TUS9509145A

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Lung Cancer Marker

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS

STREET: 1201 Elm street, Suite 4500

CITY: Dallas

STATE: TX

COUNTRY: US

ZIP: 75270-2197

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/09145A

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: John A. Harre

REGISTRATION NUMBER: 37,345

REFERENCE/DOCKET NUMBER: B35792CIPCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 214-939-4500

TELEFAX: 214-939-4600

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 325 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-09145A-4

Query Match

Best Local Similarity 59.5%; Score 47; DB 4; Length 325;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
 1111 1111
 Db 96 PNDPHGSEHT 105

RESULT 11

PCT-US95-09145A-18
 ; Sequence 18, Application PC/TUS9509145A
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Lung Cancer Marker
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
 ; STREET: 1201 Elm Street, Suite 4500
 ; CITY: Dallas
 ; STATE: TX
 ; COUNTRY: US
 ; ZIP: 75270-2197
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/09145A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: John A. Harre
 ; REGISTRATION NUMBER: 37,345
 ; REFERENCE/DOCKET NUMBER: B35792CIPCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 214-939-4500
 ; TELEFAX: 214-939-4600
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 325 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US95-09145A-18

Query Match 59.5%; Score 47; DB 4; Length 325;
 Best Local Similarity 80.0%; Pred. No. 1.5;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
 1111 1111
 Db 96 PNDPHGSEHT 105

RESULT 12

US-08-276-919-2
 ; Sequence 2, Application US/08276919
 ; Patent No. 5589579
 ; GENERAL INFORMATION:
 ; APPLICANT: Torczynski, Richard M.
 ; APPLICANT: Bollon, Arthur P.
 ; TITLE OF INVENTION: Lung Cancer Marker
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
 ; STREET: 1201 Elm Street, Suite 4500
 ; CITY: Dallas
 ; STATE: TX
 ; COUNTRY: US
 ; ZIP: 75270-2197
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/276,919
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Nelligan, Mark C.
 ; REGISTRATION NUMBER: 36,389
 ; REFERENCE/DOCKET NUMBER: B35792
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 214-939-4500
 ; TELEFAX: 214-939-4600
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 354 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-276-919-2

Query Match 59.5%; Score 47; DB 1; Length 354;
 Best Local Similarity 80.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
 1111 1111
 Db 125 PNDPHGSEHT 134

RESULT 13
 US-08-776-088-2
 ; Sequence 2, Application US/08776088
 ; Patent No. 5773579
 ; GENERAL INFORMATION:
 ; APPLICANT: Torczynski, Richard M.
 ; APPLICANT: Bollon, Arthur P.
 ; TITLE OF INVENTION: Lung Cancer Marker
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SIDLEY & AUSTIN
 ; STREET: 1201 Elm Street, Suite 4500
 ; CITY: Dallas
 ; STATE: TX
 ; COUNTRY: US
 ; ZIP: 75270-2197
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/776,088
 ; FILING DATE: 19-JUL-95
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Eugenia S. Hansen
 ; REGISTRATION NUMBER: 31,966
 ; REFERENCE/DOCKET NUMBER: 10365/05011
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 214-981-3300
 ; TELEFAX: 214-981-3400
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 354 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-776-088-2

Query Match 59.5%; Score 47; DB 1; Length 354;
 Best Local Similarity 80.0%; Pred. No. 1.7;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 PNDPASEHT 13
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Db 125 PNDPASEHT 134

RESULT 14
US-08-776-088-6
; Sequence 6, Application US/08776088
; Patent No. 5773579
; GENERAL INFORMATION:
; APPLICANT: Torczynski, Richard M.
; APPLICANT: Bollion, Arthur P.
; TITLE OF INVENTION: Lung Cancer Marker
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STIDLEY & AUSTIN
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: TX
; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,088
; FILING DATE: 19-JUL-95
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Eugenia S. Hansen
; REGISTRATION NUMBER: 31,966
; REFERENCE/DOCKET NUMBER: 10365/05011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 214-981-3400
; TELEFAX: 214-981-3300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-776-088-6

Query Match 59.5%; Score 47; DB 1; Length 354;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PNDPASEHT 13
 |||||
Db 125 PNDPASEHT 134

RESULT 15
US-09-325-320-2
; Sequence 2, Application US/09325320
; Patent No. 6117981
; GENERAL INFORMATION:
; APPLICANT: Torczynski, Richard M.
; APPLICANT: Bollion, Arthur P.
; TITLE OF INVENTION: HYBRIDOMAS FOR LUNG CANCER MARKER AND MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES THEREOF
; FILE REFERENCE: 10365/06101
; CURRENT APPLICATION NUMBER: US/09/325,320
; CURRENT FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 354

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-325-320-2

Query Match 59.5%; Score 47; DB 3; Length 354;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 PNDPASEHT 13
 |||||
Db 125 PNDPASEHT 134

Search completed: February 2, 2001, 10:36:30
Job time: 43 sec

Fri Feb 2 15:15:35 2001

us-09-273-217-3.ra1

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 2, 2001, 10:36:30 ; Search time 34.98 Seconds
(without alignments)
7.700 Million cell updates/sec

Title: US-09-273-217-4
Perfect score: 78
Sequence: 1 FAHADPTSGFSSIP 15

Scoring table:
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Gapop 10.0 , Gapept 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	91.0	528	2	US-08-527-152-2
2	43	55.1	597	1	US-08-462-884A-1
3	43	55.1	597	1	US-08-461-881B-1
4	43	55.1	597	2	US-09-123-960-1
5	43	55.1	605	1	US-08-462-884A-3
6	43	55.1	605	1	US-08-461-881B-3
7	43	55.1	605	2	US-09-123-960-3
8	41	52.6	78	2	US-08-624-123-13
9	41	52.6	78	2	US-08-716-308-2
10	41	52.6	78	2	US-08-716-308-16
11	41	52.6	78	4	PCT-US96-05262-14
12	41	52.6	617	1	US-08-191-866D-58
13	41	52.6	617	2	US-08-185-949B-58
14	40	51.3	535	1	US-08-445-050-4
15	40	51.3	535	2	US-08-204-691-4
16	40	51.3	539	1	US-08-464-340A-13
17	40	51.3	546	1	US-08-445-050-5
18	40	51.3	546	2	US-08-204-691-5
19	40	51.3	568	2	US-08-445-050-6
20	40	51.3	568	2	US-08-204-691-6
21	40	51.3	521	5	5200183-17
22	40	51.3	668	1	US-08-445-050-9
23	40	51.3	668	2	US-08-204-691-9
24	40	51.3	722	1	US-08-347-718B-1
25	40	51.3	722	1	US-08-445-050-3
26	40	51.3	722	1	US-08-445-050-7
27	40	51.3	722	2	US-08-482-262-1
28	40	51.3	722	2	US-08-204-691-3

29	40	51.3	722	2	US-08-204-691-7	Sequence 7, Appli
30	40	51.3	722	5	5200183-3	Patent No. 5200183
31	40	51.3	742	1	US-08-347-718B-2	Sequence 2, Appli
32	40	51.3	742	2	US-08-482-262-2	Sequence 2, Appli
33	40	51.3	742	5	5200183-2	Patent No. 5200183
34	40	51.3	745	1	US-08-445-050-2	Sequence 2, Appli
35	40	51.3	745	2	US-08-204-691-2	Sequence 2, Appli
36	40	51.3	745	3	US-08-370-223-13	Sequence 13, Appli
37	39	50.0	51	1	US-07-689-693B-21	Sequence 21, Appli
38	39	50.0	78	1	US-07-689-693B-5	Sequence 5, Appli
39	39	50.0	723	5	5200183-4	Patent No. 5200183
40	37	47.4	532	1	US-08-288-405A-10	Sequence 10, Appli
41	37	47.4	615	2	US-08-738-349-12	Sequence 12, Appli
42	37	47.4	693	2	US-08-738-349-6	Sequence 6, Appli
43	37	47.4	796	1	US-08-188-228-58	Sequence 58, Appli
44	37	47.4	796	1	US-08-332-643-52	Sequence 52, Appli
45	37	47.4	796	1	US-08-332-638-58	Sequence 58, Appli

ALIGNMENTS

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RESULT 1
US-08-527-152-2
; Sequence 2, Application US/08527152
; Patent No. 5827655
;
; GENERAL INFORMATION:
; APPLICANT: Chandu, Kanianthara G.
; APPLICANT: Cahalan, Michael D.
; APPLICANT: Grissmer, Stephan
; APPLICANT: Goldin, Alan L.
; APPLICANT: Guthrie, Brent A.
; APPLICANT: Gutman, George A.
; APPLICANT: Masumth, John J.
; TITLE OF INVENTION: Assay, Methods and Products Based On n
; TITLE OF INVENTION: K+ Channel Expression
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/527,152
; FILING DATE: UNKNOWN
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/170,418
; FILING DATE: 20-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/558,568
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-54444-2/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 528 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-08-527-152-2

Query Match 91.0%; Score 71; DB 2; Length 528;
Best Local Similarity 86.7%; Pred. No. 3,2e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEADPTSGFSSIP 15
Db 371 FAEADPTSGFSSIP 385

RESULT 2
US-08-462-884A-1
; Sequence 1, Application US/08462884A
; Patent No. 5624836
; GENERAL INFORMATION:
; APPLICANT: Lange III, Louis G
; APPLICANT: Spilburg, Curtis A
; TITLE OF INVENTION: Mammalian Pancreatic Cholesterol
; TITLE OF INVENTION: Esterase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Banner & Allegretti
; STREET: 10 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,884A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Blair Hughes
; REGISTRATION NUMBER: 32,901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/715-1000
; TELEFAX: 312/715-1234
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..597
; OTHER INFORMATION: /note="Bovine pancreatic
; OTHER INFORMATION: cholesterol esterase"
US-08-462-884A-1

Query Match 55.1%; Score 43; DB 1; Length 597;
Best Local Similarity 46.7%; Pred. No. 5.4;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 FAEADPTSGFSSIP 15
Db 489 FARTGDPWGHSTVP 503

RESULT 3
US-08-461-881B-1
; Sequence 1, Application US/08461881B

; Patent No. 5792832
; GENERAL INFORMATION:
; APPLICANT: Lange III, Louis G
; APPLICANT: Spilburg, Curtis A
; TITLE OF INVENTION: Mammalian Pancreatic Cholesterol Esterase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" hard disc
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,881B
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Blair Hughes
; REGISTRATION NUMBER: 32,901
; REFERENCE/DOCKET NUMBER: 89,852-J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/913-0001
; TELEFAX: 312/913-0002
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..597
; OTHER INFORMATION: /note="Bovine pancreatic
; OTHER INFORMATION: cholesterol esterase"
US-08-461-881B-1

Query Match 55.1%; Score 43; DB 1; Length 597;
Best Local Similarity 46.7%; Pred. No. 5.4;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 FAEADPTSGFSSIP 15
Db 489 FARTGDPWGHSTVP 503

RESULT 4
US-09-123-960-1
; Sequence 1, Application US/09123960
; Patent No. 5981299
; GENERAL INFORMATION:
; APPLICANT: Lange III, Louis G
; APPLICANT: Spilburg, Curtis A
; TITLE OF INVENTION: Mammalian Pancreatic
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" hard disc
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/123,960
APPLICATION NUMBER: 32,901
FILING DATE: 1995
CLASSIFICATION: 32,901
PRIOR APPLICATION DATA: 89,852-K
APPLICATION NUMBER: 08/461,881
FILING DATE: June 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: A. Blair Hughes
REGISTRATION NUMBER: 32,901
REFERENCE/DOCKET NUMBER: 89,852-K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/913-0001
TELEFAX: 312/913-0002
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 597 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..597
OTHER INFORMATION: /note="Bovine pancreatic
OTHER INFORMATION: cholesterol esterase"
US-09-123-960-1

Query Match 55.1%; Score 43; DB 2; Length 597;
Best Local Similarity 46.7%; Pred. No. 5.4;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 FAADDPTSGFSSIP 15
DB 489 FARTGDPNTGHSVP 503

RESULT 5
US-08-462-884A-3
Sequence 3, Application US/08462884A
Patent No. 5624836
GENERAL INFORMATION:
APPLICANT: Lange III, Louis G
APPLICANT: Spilburg, Curtis A
TITLE OF INVENTION: Mammalian Pancreatic Cholesterol
TITLE OF INVENTION: Esterase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti
STREET: 10 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,884A
FILING DATE: Unknown
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: A. Blair Hughes
REGISTRATION NUMBER: 32,901
REFERENCE/DOCKET NUMBER: 89,852-J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/715-1000
TELEFAX: 312/715-1234
TELEX: 910/221-5317

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-884A-3

Query Match 55.1%; Score 43; DB 1; Length 605;
Best Local Similarity 46.7%; Pred. No. 5.4;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 FAADDPTSGFSSIP 15
DB 497 FARTGDPNTGHSVP 511

RESULT 6
US-08-461-881B-3
Sequence 3, Application US/08461881B
Patent No. 5792832
GENERAL INFORMATION:
APPLICANT: Lange III, Louis G
APPLICANT: Spilburg, Curtis A
TITLE OF INVENTION: Mammalian Pancreatic
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" hard disc
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,881B
FILING DATE: June 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: A. Blair Hughes
REGISTRATION NUMBER: 32,901
REFERENCE/DOCKET NUMBER: 89,852-J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/913-0001
TELEFAX: 312/913-0002
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-881B-3

Query Match 55.1%; Score 43; DB 1; Length 605;
Best Local Similarity 46.7%; Pred. No. 5.4;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 FAADDPTSGFSSIP 15
DB 497 FARTGDPNTGHSVP 511

RESULT 7
US-09-123-960-3
Sequence 3, Application US/09123960
Patent No. 5981299

GENERAL INFORMATION:
APPLICANT: Lange III, Louis G
APPLICANT: Spilburg, Curtis A
TITLE OF INVENTION: Mammalian Pancreatic
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" hard disc
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,960
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,881
FILING DATE: June 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: A. Blair Hughes
REGISTRATION NUMBER: 32,901
REFERENCE/DOCKET NUMBER: 89,852-K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/913-0001
TELEFAX: 312/913-0002
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-123-960-3

Query Match 55.1%; Score 43; DB 2; Length 605;
Best Local Similarity 46.7%; Pred. No. 5.4;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 FAADDPGSGSSIP 15
Db 497 FARTGDPNGHSTYP 511

RESULT 8
US-08-624-123-13
Sequence 13, Application US/08624123
Patent No. 5739276
GENERAL INFORMATION:
APPLICANT: Shon, Ki-Joon
APPLICANT: Grille, Michelle M.
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/624,123
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,554
FILING DATE: 07-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/423,561
FILING DATE: 17-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107674-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
US-08-624-123-13

Query Match 52.6%; Score 41; DB 1; Length 78;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 FAADDPGSGSSIP 14
Db 19 FARTDPPRNGHNT 32

RESULT 9
US-08-716-308-2
Sequence 2, Application US/08716308
Patent No. 5885569
GENERAL INFORMATION:
APPLICANT: Windass, John D.
TITLE OF INVENTION: Biological Insect Control Agent
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENeca Inc.
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,308
FILING DATE: 24-SEP-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00677
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9405951.6
FILING DATE: 23-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschultz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD40027X/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-716-308-2

Query Match 52.6%; Score 41; DB 2; Length 78;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 FARADPTSGFSSI 14
DB 19 FARADPTSGFSSI 32

RESULT 10

US-08-716-308-16
Sequence 16, Application US/08716308
Patent No. 5885369
GENERAL INFORMATION:
APPLICANT: Windass, John D.
TITLE OF INVENTION: Biological Insect Control Agent
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENECA Inc.
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,308
FILING DATE: 24-SEP-1996
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00677
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9405951.6
FILING DATE: 25-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD40027X/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ. ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-716-308-16

Query Match 52.6%; Score 41; DB 2; Length 78;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 FARADPTSGFSSI 14
DB 19 FARADPTSGFSSI 32

RESULT 11
PCT-US96-05262-14

Sequence 14, Application PC/TUS9605262

GENERAL INFORMATION:
APPLICANT: Shon, Ki-Joon
APPLICANT: Grilley, Michelle M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Yoshikami, Doju
APPLICANT: Marsh, Maren
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05262
FILING DATE: 17-APR-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/423,561
FILING DATE: 17-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 24260-107674
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
TELEFAX: 202-962-8300
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
PCT-US96-05262-14

Query Match 52.6%; Score 41; DB 4; Length 78;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 FARADPTSGFSSI 14
DB 19 FARADPTSGFSSI 32

RESULT 12

US-08-191-866D-58
Sequence 58, Application US/08191866D
Patent No. 5783195
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Macdonald, Richard D.
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Rhinotracheitis Virus S-IBR-052 And Uses Thereof
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,866D
FILING DATE: 4 February 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 617 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-191-866D-58

Query Match 52.6%; Score 41; DB 1; Length 617;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 AADDPGSGFSSIP 15
DB 558 AGAPEPTSGFARAP 571

RESULT 13
US-08-185-949B-58
Sequence 58, Application US/08185949B
Patent No. 5874279
GENERAL INFORMATION:
APPLICANT: Mark D. Cochran
TITLE OF INVENTION: Recombinant Infectious Bovine
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,949B
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 278-0525
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 617 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-185-949B-58

Query Match 52.6%; Score 41; DB 2; Length 617;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 AADDPGSGFSSIP 15
DB 558 AGAPEPTSGFARAP 571

RESULT 14
US-08-445-050-4
Sequence 4, Application US/08445050
Patent No. 5763739
GENERAL INFORMATION:
APPLICANT: Blaeckberg, Lars
APPLICANT: Edlund, Michael
APPLICANT: Hansson, Lennart
APPLICANT: Herneli, Olle
APPLICANT: Lundberg, Lennart
APPLICANT: Stromqvist, Mats
APPLICANT: Toernell, Jan
TITLE OF INVENTION: No. 5763739el Polypeptides
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,050
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/204,691
FILING DATE:
APPLICATION NUMBER: SE 9300686-4
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300722-7
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sterner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Mammary gland
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..535
OTHER INFORMATION: /label= Variant_A
US-08-445-050-4

Query Match 51.3%; Score 40; DB 1; Length 535;
 Best Local Similarity 46.7%; Pred. No. 17;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 FAADDPPTSGFSSIP 15
 ||: || | : : |
 Db 471 FAKTGDPMNGDSAVP 485

QY 1 FAADDPPTSGFSSIP 15
 ||: || | : : |
 Db 471 FAKTGDPMNGDSAVP 485
 Search completed: February 2, 2001, 10:36:31
 Job time: 44 sec

RESULT 15
 US-08-204-691-4
 ; Sequence 4, Application US/08204691
 ; Patent No. 5827683
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaeckberg, Lars
 ; APPLICANT: Edlund, Michael
 ; APPLICANT: Hansson, Lennart
 ; APPLICANT: Herneil, Olle
 ; APPLICANT: Lundberg, Lennart
 ; APPLICANT: Stroemqvist, Mats
 ; APPLICANT: Toernell, Jan
 ; TITLE OF INVENTION: No. 5827683el Polypeptides
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: White & Case
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 10036-2787
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/204,691
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: SE 9300686-4
 ; FILING DATE: 01-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: SE 9300722-7
 ; FILING DATE: 04-MAR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Steiner Ph.D., Richard J
 ; REGISTRATION NUMBER: 35,372
 ; REFERENCE/DOCKET NUMBER: 1103326-850
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212)819-8783
 ; TELEFAX: (212)354-8113
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 535 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; TISSUE TYPE: Mammary gland
 ; FEATURE:
 ; NAME/KEY: Peptide
 ; LOCATION: 1..535
 ; OTHER INFORMATION: /label= Variant_A
 ; US-08-204-691-4

Query Match 51.3%; Score 40; DB 2; Length 535;
 Best Local Similarity 46.7%; Pred. No. 17;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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